

## HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

### Cross Reference to Related Applications

5 This application claims priority to the following provisional applications: U.S.  
Ser. No. 60/188,914, filed March 13, 2000, entitled, "NOVEL OLFACTORY  
RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No.  
60/192,033, filed March 24, 2000, entitled, "NOVEL OLFACTORY RECEPTORS  
AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/198,474, filed  
10 April 12, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENE  
ENCODING THE SAME" to Zozulya; U.S. Ser. No. 60/199,335, filed April 24, 2000,  
"HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to  
Zozulya; U.S. Ser. No. 60/207,702, filed May 26, 2000, entitled, "HUMAN  
OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya;  
15 U.S. Ser. No. 60/213,849, filed June 23, 2000, entitled, "HUMAN OLFACTORY  
RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No.  
60/226,534, filed August 16, 2000, "HUMAN OLFACTORY RECEPTORS AND  
GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/230,732, filed  
September 7, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES  
ENCODING THE SAME", to Zozulya; and U.S. Ser. No. 60/266,862, filed February  
20 7, 2001, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE  
SAME", to Zozulya. All of these applications are herein incorporated by reference in  
their entirety.

### Field of the Invention

25 The invention relates to newly identified mammalian chemosensory G protein-  
coupled receptors, particularly olfactory receptors, fragments thereof, classes of such  
receptors, genes and cDNAs encoding said receptors, vectors including said receptors,  
and cells that express said receptors. The invention also relates to methods of using  
such receptors, fragments, genes, cDNAs, vectors, and cells to identify molecules  
30 involved in olfactory perception. The invention therefore has application in the  
selection and design of odorant compositions, as well as malodor blockers (olfactory  
receptor antagonists), particularly perfumes and fragrance compositions and  
components of deodorants and other malodor blocking compositions.

### Description of the Related Art

The olfactory system provides sensory information about the chemical composition of the external world. Olfactory sensation is thought to involve distinct signaling pathways. These pathways are believed to be mediated by olfactory receptors (ORs). Cells which express olfactory receptors, when exposed to certain chemical stimuli, elicit olfactory sensation by depolarizing to generate an action potential, which is believed to trigger the sensation.

As such, olfactory receptors specifically recognize molecules that elicit specific olfactory sensation. These molecules are also referred to herein as "odorants." Olfactory receptors belong to the 7-transmembrane receptor superfamily (Buck *et al.*, *Cell* 65:175-87 (1991)), which are also known as G protein-coupled receptors (GPCRs). G protein-coupled receptors control many physiological functions, such as endocrine function, exocrine function, heart rate, lipolysis, carbohydrate metabolism, and transmembrane signaling. The biochemical analysis and molecular cloning of a number of such receptors has revealed many basic principles regarding the function of these receptors.

For example, U. S. Patent No. 5,691,188 describes how upon a ligand binding to a GPCR, the receptor presumably undergoes a conformational change leading to activation of the G protein. G proteins are comprised of three subunits: a guanyl nucleotide binding  $\alpha$  subunit, a  $\beta$  subunit, and a  $\gamma$  subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the  $\alpha$  subunit. When GDP is bound, the G protein exists as a heterotrimer: the  $G\alpha\beta\gamma$  complex. When GTP is bound, the  $\alpha$  subunit dissociates from the heterotrimer, leaving a  $G\beta\gamma$  complex. When a  $G\alpha\beta\gamma$  complex operatively associates with an activated G protein-coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of dissociation of the bound  $G\alpha$  subunit from the  $G\alpha\beta\gamma$  complex increases. The free  $G\alpha$  subunit and  $G\beta\gamma$  complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell.

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel, *Sci. Amer.*, 273:154-59 (1995)). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer, *Semin. Cell Biol.*, 5:25-32 (1994)). The human genome contains approximately one thousand genes that encode a diverse repertoire of olfactory receptors (Rouquier, *Nat. Genet.*, 18:243-50 (1998); Trask, *Hum. Mol. Genet.*, 7:2007-20 (1998)). It has been demonstrated that members of the OR gene family are distributed on all but a few human chromosomes. Through fluorescence *in situ* hybridization analysis, Rouquier showed that OR sequences reside at more than 25 locations in the human genome. Rouquier also determined that the human genome has accumulated a striking number of dysfunctional OR copies: 72% of the analyzed sequences were found to be pseudogenes. An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic tastants or odorants, is complicated by the fact that chemosensory receptors belong to a multigene family with over a thousand members. For instance, there are up to 1,000 odorant receptors in mammals.

Moreover, each chemosensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it expresses. To analyze odorant-receptor interactions and their effects on olfactory cells, specific ligands and the olfactory receptors to which they bind are identified. This analysis requires isolation and expression of olfactory polypeptides, followed by binding assays.

Some studies suggest that OR genes can be expressed in tissues other than the olfactory epithelium, indicating potential alternative biological roles for this class of chemosensory receptors. Expression of various ORs has been reported in human and murine erythroid cells (Feingold 1999), developing rat heart (Drutel, *Receptor Channels*, 3(1):33-40 (1995)), avian notochord (Nef, *PNAS*, 94(9):4766-71 (1997)) and lingual epithelium (Abe, *FES Lett.*, 316(3):253-56 (1993)). One experimentally documented case also established the existence of a large subset of mammalian ORs transcribed in testes and expressed on the surface of mature spermatozoa, thereby

suggesting a possible role of ORs in sperm chemotaxis (Parmenthler, *Nature*, 355:453-55 (1992); Walensky, *Mol. Med.*, 1(2):130-41 (1998); Branscomb, *Genetics*, 156(2):785-97 (2000)). It was also hypothesized that olfactory receptors might provide molecular codes for highly specific cell-cell recognition functions in development and embryogenesis (Dreyer, *PNAS*, 95(11):9072-77 (1998)).

Complete or partial sequences of numerous human and other eukaryotic chemosensory receptors are currently known. See, e.g., Pilpel, Y. and Lancet, D., *Protein Science*, 8:969-77 (1999); Mombaerts, P., *Annu. Rev. Neurosci.*, 22:487-50 (1999); see also, EP0867508A2, US 5874243, WO 92/17585, WO 95/18140, WO 97/17444, WO 99/67282. Due to the complexity of ligand-receptor interactions, and more particularly odorant-receptor interactions, information about ligand-receptor recognition is lacking. In part, the present invention addresses the need for better understanding of these interactions. The present invention also provides, among other things, novel chemosensory receptors, and methods for utilizing such novel chemosensory receptors and the genes and cDNAs encoding such receptors, especially for identifying compounds that can be used to module chemosensory transduction, such as olfaction.

#### Summary of the Invention

Toward that end, it is an object of the invention to provide a new family of G protein-coupled receptors comprising over two hundred fifty olfactory G protein-coupled receptors (OR) active in olfactory perception. It is another object of the invention to provide fragments and variants of such ORs which retain odorant-binding activity.

It is yet another object of the invention to provide nucleic acid sequences or molecules that encode such ORs, fragments, or allelic variants.

It is still another object of the invention to provide expression vectors which include nucleic acid sequences that encode such ORs, or fragments, or variants thereof, which are operably linked to at least one regulatory sequence such as a promoter, enhancer, or other sequences involved in positive or negative gene transcription and/or translation.

It is still another object of the invention to provide human or non-human cells that functionally express at least one of such ORs, or fragments, or variants thereof.

It is still another object of the invention to provide OR fusion proteins or polypeptides which include at least a fragment of at least one of such ORs.

It is another object of the invention to provide an isolated nucleic acid molecule encoding an OR comprising a nucleic acid sequence that is at least 30%,  
5 more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from the group consisting of: SEQ. ID. NO. 2, SEQ. ID. NO. 4, SEQ. ID. NO. 6, SEQ. ID. NO. 8, SEQ. ID. NO. 10, SEQ. ID. NO. 12, SEQ. ID. NO. 14, SEQ. ID. NO. 16, SEQ. ID. NO. 18, SEQ. ID. NO. 20, SEQ. ID.  
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SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID  
NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512.

It is a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence which is at least 40%, more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID.

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499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ  
ID NO: 509 and SEQ ID NO: 511.



It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO. 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251, SEQ. ID. NO. 253,

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 10 ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID. NO. 337, SEQ. ID.  
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 20 SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ. ID. NO. 423, SEQ.  
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 25 ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID.  
 NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO.  
 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483,  
 SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ.  
 ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO:  
 30 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and  
 SEQ ID NO: 511, wherein the fragment is at least 10, preferably 20, 30, 50, 70, 100,  
 or 150 amino acids in length.

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a variant of said fragment, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

- 5        It is still another object of the invention to provide an isolated polypeptide comprising an amino acid sequence that is at least 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, 15    SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID.

NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID.  
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5 SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.  
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20 SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ.  
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SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ.  
25 ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID.  
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30 NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO.  
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ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:

499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

It is still a further object of the invention to provide an isolated polypeptide comprising a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.

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 10 SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ.  
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 20 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413,  
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 25 SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ.  
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 SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ.  
 30 ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:  
 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ  
 ID NO: 509 and SEQ ID NO: 511, wherein the fragment is at least 40, preferably 60,  
 80, 100, 150, 200, or 250 amino acids in length.

It is still a further object of the invention to provide an isolated polypeptide comprising a variant of said fragment, especially naturally occurring allelic variants, the expression of which may be significant in the manner by which different persons in the human population perceive odors differently, both on a qualitative and  
5 quantitative level, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

It is still another object of the invention to provide agonists, including inverse agonists, or antagonists of such ORs, or fragments or variants thereof.

It is yet another object of the invention to provide methods for representing the  
10 perception of odor and/or for predicting the perception of odor in a mammal, including in a human. Preferably, such methods may be performed by using the ORs, or fragments or variants thereof, and genes encoding such ORs, or fragments or variants thereof, disclosed herein.

It is yet another object of the invention to provide novel molecules or combinations of  
15 molecules which elicit a predetermined olfactory perception in a mammal. Such molecules or compositions can be generated by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules; comparing the value of olfactory perception  
20 in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a  
25 predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

It is still a further object of the invention to provide a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising:  
30 a step of contacting said one or more compounds with the disclosed ORs, fragments or variants thereof, preferably wherein the mammal is a human.

It is another object of the invention to provided a method for simulating a fragrance, comprising: for each of a plurality of ORs, or fragments of variants thereof

disclosed herein, preferably human ORs, ascertaining the extent to which the OR interacts with the fragrance; and combining a plurality of compounds, each having a previously ascertained interaction with one or more of the ORs, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an OR can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80% or 90% or all of the receptors that are substantially stimulated by the fragrance.

In yet another aspect of the invention, a method is provided wherein a plurality of standard compounds are tested against a plurality of ORs, or fragments or variants thereof, to ascertain the extent to which the ORs each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

It is a further object of the invention to provide a method for representing olfactory perception of a particular smell in a mammal, comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  ORs of said vertebrate, where  $n$  is greater than or equal to 4,  $n$  is greater than or equal to 12;  $n$  is greater than or equal to 24,  $n$  is greater than or equal to 48;  $n$  is greater than or equal to 72;  $n$  is greater than or equal to 96;  $n$  is greater than or equal to 120;  $n$  is greater than or equal to 144;  $n$  is greater than or equal to 168;  $n$  is greater than or equal to 192;  $n$  is greater than or equal to 216, or  $n$  is greater than or equal to 256; and generating from said values a quantitative representation of olfactory perception. The ORs may be an olfactory receptor disclosed herein, or fragments or variants thereof, the representation may constitutes a point or a volume in  $n$ -dimensional space, may constitutes a graph or a spectrum, and may constitutes a matrix of quantitative representations. Also, the



providing step may comprise contacting a plurality of recombinantly produced ORs, or fragments or variants thereof, with a test composition and quantitatively measuring the interaction of said composition with said receptors.

- It is yet another object of the invention to provide a method for predicting the
- 5 olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  ORs of said vertebrate, where  $n$  is greater than or equal to 4  $n$  is greater than or equal to 12;  $n$  is greater than or equal to 24,  $n$  is greater than or equal to 48;  $n$  is
- 10 greater than or equal to 72;  $n$  is greater than or equal to 96;  $n$  is greater than or equal to 120;  $n$  is greater than or equal to 144;  $n$  is greater than or equal to 168;  $n$  is greater than or equal to 192;  $n$  is greater than or equal to 216, or  $n$  is greater than or equal to 256; for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative
- 15 representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  ORs of said vertebrate, where  $n$  is greater than or equal to 4,  $n$  is greater than or equal to 12;  $n$  is greater than or equal to 24,  $n$  is greater than or equal to 48;  $n$  is greater than
- 20 or equal to 72;  $n$  is greater than or equal to 96;  $n$  is greater than or equal to 120;  $n$  is greater than or equal to 144;  $n$  is greater than or equal to 168;  $n$  is greater than or equal to 192;  $n$  is greater than or equal to 216, or  $n$  is greater than or equal to 273; for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of
- 25 olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by
- 30 comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known

olfactory perception in a mammal. The ORs used in this method may include an olfactory receptor, or fragment or variant thereof, disclosed herein.

#### Brief Description of the Drawings

5           Figure 1 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR1 through AOLFR52. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences  
10 AOLFR2 through AOLFR52 were analyzed for alignment with the AOLFR1 amino acid sequence.

          Figure 2 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins  
15 described herein are designated AOLFR54 through AOLFR109. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR55 through AOLFR109 were analyzed for alignment with the AOLFR54 amino acid sequence.

          Figure 3 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins  
20 described herein are designated AOLFR110 through AOLFR163. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR111 through AOLFR163 were analyzed for alignment with the  
25 AOLFR110 amino acid sequence.

          Figure 4 illustrates the multiple sequence alignment derived for fifty-four novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-four novel human olfactory receptors (hOR) proteins described herein are designated AOLFR165 through AOLFR217. The  
30 alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR166 through AOLFR217 were analyzed for alignment with the AOLFR165 amino acid sequence.

Figure 5 illustrates the multiple sequence alignment derived for fifty-two novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-two novel human olfactory receptors (hOR) proteins described herein, which are designated AOLFR218 through AOLFR328. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR219 through AOLFR328 were analyzed for alignment with the AOLFR218 amino acid sequence.

#### Detailed Description of the Invention

The invention thus provides isolated nucleic acid molecules encoding olfactory-cell-specific G protein-coupled receptors ("GPCRs"), and the polypeptides they encode. These nucleic acid molecules and the polypeptides that they encode are members of the olfactory receptor family. Other members of the olfactory receptor family are disclosed in Krautwurst, *et al.*, *Cell*, 95:917-26 (1998), and WO 0035274, the contents of which are herein incorporated by reference in their entireties.

According to one aspect of the invention, genes encoding over two hundred fifty distinct, novel human olfactory (odorant) receptors (also herein referred to ORs) have been identified in genome sequence databases. All of these receptor genes have been initially detected by computer DNA sequence analysis of genomic clones (unfinished High Throughput Genomic Sequence database accession numbers AB045359, AP002532, AP002533, AL365440, AC073487, AL359636, AL359955, AP002535, AB045365, AL359218, AC002555, AB045361, AL359512, AC023255, AL358773, AL357767, AL358874, AC068380, AC025283, AP002407, AC018700, AC022289, AC006313, AC002556, AC011571, AL121944, AC007194, AP001112, AC021660, AP000723, AC016856, AC018700, AP000818, AC00596, AP000916, AC011517, AP001112, AP000916, AC021427, AC021427, AC020884, AC019108, AL135841, AL133410, AF186996, AL138834, AC009237, AC025249, AC010930, AC009758, AC009642, AC009758, AC025249, AF101706, AC009642, AC025249, AC021660, AC011647, AC011711, AC009642, AC020597, AC011711, AC019088, AC022882, AC011571, AL121944, AP000435, AC012616, AC010332, AC010766, AP000743, AC021809, AC011879, AC021304, AC023226, AL160314, AC021304, AC020380, AC011904, AC004977, AC021304, AP000868, AP000825, AC023080, AC022207, AC121986, AC010814, AC018700, AC021304, AC008620, AC011537,

AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, AP001803, AP001804, AL353767, AP001884, AC026083, 5 AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, AP002826, AL359636, AL391534, AC055731, AC076959, 10 AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes.

Alternatively, nucleic acids encoding the olfactory receptors (ORs) and polypeptides of the invention can be isolated from a variety of sources, genetically 15 engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 0035374, which is herein incorporated by reference in its entirety.

These nucleic acids provide valuable probes for the identification of olfactory cells, as the nucleic acids are specifically expressed in olfactory cells. They can also 20 serve as tools for the generation of sensory topographical maps that elucidate the relationship between olfactory cells and olfactory sensory neurons leading to olfactory centers in the brain. Furthermore, the nucleic acids and the polypeptides they encode can be used as probes to elucidate olfactory-induced behaviors.

The invention also provides methods of screening for modulators, *e.g.*, 25 activators, inhibitors, stimulators, enhancers, agonists, inverse agonists and antagonists, of the ORs, or fragments or variants thereof, of the invention. Such modulators of olfactory transduction are useful for pharmacological and genetic modulation of olfactory signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of olfactory cell activity. These 30 modulator compounds can then be used in the food, pharmaceutical, and cosmetic industries to customize odors and fragrances.

Thus, the invention provides assays for olfactory modulation, where the ORs, or fragments or variants thereof, of the invention act as direct or indirect reporter

5 molecules for the effect of modulators on olfactory transduction. The ORs, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo* and *ex vivo*. In one embodiment, the ORs, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g.*, Mistili *et al.*, *Nature Biotech.*, 15:961-64 (1997)). In another embodiment, the ORs, or fragments or variants thereof, can be expressed in host cells, and modulation of olfactory transduction via OR activity can be assayed by measuring changes in  $\text{Ca}^{2+}$  levels.

10 Methods of assaying for modulators of olfactory transduction include *in vitro* ligand binding assays using the ORs of the invention, or fragments or variants thereof. More particularly, such assays can use the ORs; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular  $\text{Ca}^{2+}$  levels; and neurotransmitter release.

15 20 The invention also provides for methods of detecting olfactory nucleic acid and protein expression, allowing for the investigation of olfactory transduction regulation and specific identification of olfactory receptor cells. The ORs, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying olfactory receptor cells. Olfactory receptor cells can be identified using techniques such as reverse transcription and amplification of mRNA, isolation of total RNA or poly A<sup>+</sup> RNA, northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, western blots, and the like.

#### **A. Identification and Characterization of Olfactory Receptors**

30 The amino acid sequences of the ORs and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various

amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window," as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of: from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *PNAS*, 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., *Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued

threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990)). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *PNAS*, 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-called "tree" or "dendrogram" showing the clustering relationships used to create the alignment (*see, e.g.*, Figure 2). PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351-60 (1987). The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple

extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using  
5 PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, e.g., version 7. 0 (Devereaux *et al.*, *Nuc. Acids Res.* 12:387-395 (1984) encoded by the genes were  
10 derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian olfactory receptor family, each of the odorant receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most  
15 preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative OR proteins generally having lengths of approximately 290 to approximately 400 amino acid residues that contain seven transmembrane domains, as  
20 predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor 7-transmembrane (7TM) superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the ORs identified herein has a characteristic sequence signature of an olfactory receptor. In particular, all the identified sequences contain very close  
25 matches to the following consensus amino acid motifs (Mombaerts, 1999, Pilpel 1999): EFILL (SEQ ID NO: 513) before transmembrane domain 1, LHTPMY (SEQ ID NO: 514) in intracellular loop 1, MAYDRYVAIC (SEQ ID NO: 510) at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5, FSTCSSH (SEQ ID NO: 516) in the beginning of  
30 transmembrane domain 6, and PMLNPF (SEQ ID NO: 517) in transmembrane domain 7. Combination of all the above-mentioned structural features of the identified genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.



As noted above, complete or partial sequences of numerous human and other eukaryotic olfactory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human olfactory receptors, which suggests their different specificity in odorant recognition. Therefore, these novel receptors and their genes can be used, alone or in combination with known olfactory receptors, in developing detection systems and assays for chemically distinct types of odorants not recognized by the known receptors, as well as for diagnostic and research purposes.

## **B. Definitions**

As used herein, the following terms have the meanings ascribed to them unless specified otherwise.

“OR” refers to one or more members of a family of G protein-coupled receptors that are expressed in olfactory cells. Olfactory receptor cells can also be identified on the basis of morphology (*see, e.g., Roper, supra*), or by the expression of proteins specifically expressed in olfactory cells. OR family members may have the ability to act as receptors for olfactory transduction.

“OR” nucleic acids encode a family of GPCRs with seven transmembrane regions that have “G protein-coupled receptor activity,” *e.g.,* they may bind to G proteins in response to extracellular stimuli and promote production of second messengers such as IP<sub>3</sub>, cAMP, cGMP, and Ca<sup>2+</sup> via stimulation of enzymes such as phospholipase C and adenylate cyclase (for a description of the structure and function of GPCRs, *see, e.g., Fong, supra*, and Baldwin, *supra*). A single olfactory cell may contain many distinct OR polypeptides.

Topologically, certain chemosensory GPCRs have an “N-terminal domain;” “extracellular domains;” “transmembrane domains” comprising seven transmembrane regions, and corresponding cytoplasmic, and extracellular loops; “cytoplasmic domains,” and a “C-terminal domain” (*see, e.g., Hoon et al., Cell*, 96:541-51 (1999); Buck & Axel, *Cell*, 65:175-87 (1991)). These domains can be structurally identified using methods known to those of skill in the art, such as sequence analysis programs that identify hydrophobic and hydrophilic domains (*see, e.g., Stryer, Biochemistry*, (3rd ed. 1988); *see also* any of a number of Internet based sequence analysis programs, such as those found at dot.imgen.bcm.tmc.edu). Such domains are useful

for making chimeric proteins and for in vitro assays of the invention, *e.g.*, ligand binding assays.

5 "Extracellular domains" therefore refers to the domains of OR polypeptides that protrude from the cellular membrane and are exposed to the extracellular face of the cell. Such domains generally include the "N terminal domain" that is exposed to the extracellular face of the cell, and optionally can include portions of the extracellular loops of the transmembrane domain that are exposed to the extracellular face of the cell, *i.e.*, the loops between transmembrane regions 2 and 3, between transmembrane regions 4 and 5, and between transmembrane regions 6 and 7.

10 The "N terminal domain" region starts at the N-terminus and extends to a region close to the start of the transmembrane domain. "Transmembrane domain," which comprises the seven "transmembrane regions," refers to the domain of OR polypeptides that lies within the plasma membrane, and may also include the corresponding cytoplasmic (intracellular) and extracellular loops. The seven  
15 transmembrane regions and extracellular and cytoplasmic loops can be identified using standard methods, as described in Kyte & Doolittle, *J. Mol. Biol.*, 157:105-32 (1982)), or in Stryer, *supra*. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus,  
20 primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below. These transmembrane domains are useful for *in vitro* ligand-binding assays, both soluble and solid phase.

25 "Cytoplasmic domains" refers to the domains of OR polypeptides that face the inside of the cell, *e.g.*, the "C terminal domain" and the intracellular loops of the transmembrane domain, *e.g.*, the intracellular loop between transmembrane regions 1 and 2, the intracellular loop between transmembrane regions 3 and 4, and the intracellular loop between transmembrane regions 5 and 6. "C terminal domain" refers to the region that spans the end of the last transmembrane domain and the C-  
30 terminus of the protein, and which is normally located within the cytoplasm.

The term "ligand-binding region" or "ligand-binding domain" refers to sequences derived from a chemosensory receptor, particularly an olfactory receptor,

that substantially incorporates at least transmembrane domains II to VII. The ligand-binding region may be capable of binding a ligand, and more particularly, an odorant.

The phrase "functional effects" in the context of assays for testing compounds that modulate OR family member mediated olfactory transduction includes the determination of any parameter that is indirectly or directly under the influence of the receptor, *e.g.*, functional, physical and chemical effects. It includes ligand binding, changes in ion flux, membrane potential, current flow, transcription, G protein binding, GPCR phosphorylation or dephosphorylation, signal transduction, receptor-ligand interactions, second messenger concentrations (*e.g.*, cAMP, cGMP, IP<sub>3</sub>, or intracellular Ca<sup>2+</sup>), *in vitro*, *in vivo*, and *ex vivo* and also includes other physiologic effects such increases or decreases of neurotransmitter or hormone release.

By "determining the functional effect" in the context of assays is meant assays for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an OR family member, *e.g.*, functional, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index), hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties, patch clamping, voltage-sensitive dyes, whole cell currents, radioisotope efflux, inducible markers, oocyte OR gene expression; tissue culture cell OR expression; transcriptional activation of OR genes; ligand-binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP, cGMP, and inositol triphosphate (IP<sub>3</sub>); changes in intracellular calcium levels; neurotransmitter release, and the like.

"Inhibitors," "activators," and "modulators" of OR genes or proteins are used interchangeably to refer to inhibitory, activating, or modulating molecules identified using *in vitro* and *in vivo* assays for olfactory transduction, *e.g.*, ligands, agonists, antagonists, and their homologs and mimetics. Inhibitors are compounds that, *e.g.*, bind to, partially or totally block stimulation, decrease, prevent, delay activation, inactivate, desensitize, or down regulate olfactory transduction, *e.g.*, antagonists. Activators are compounds that, *e.g.*, bind to, stimulate, increase, open, activate, facilitate, enhance activation, sensitize, or up regulate olfactory transduction, *e.g.*, agonists. Modulators include compounds that, *e.g.*, alter the interaction of a receptor

with: extracellular proteins that bind activators or inhibitor (*e.g.*, ebnerin and other members of the hydrophobic carrier family); G proteins; kinases (*e.g.*, homologs of rhodopsin kinase and beta adrenergic receptor kinases that are involved in deactivation and desensitization of a receptor); and arrestins, which also deactivate and desensitize receptors. Modulators can include genetically modified versions of OR family members, *e.g.*, with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, small chemical molecules and the like. Such assays for inhibitors and activators include, *e.g.*, expressing OR family members in cells or cell membranes, applying putative modulator compounds, in the presence or absence of tastants, *e.g.*, sweet tastants, and then determining the functional effects on olfactory transduction, as described above. Samples or assays comprising OR family members that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of modulation. Control samples (untreated with modulators) are assigned a relative OR activity value of 100%. Inhibition of a OR is achieved when the OR activity value relative to the control is about 80%, optionally 50% or 25-0%. Activation of an OR is achieved when the OR activity value relative to the control is 110%, optionally 150%, optionally 200-500%, or 1000-3000% higher.

The terms "purified," "substantially purified," and "isolated" as used herein refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the

meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

5 As used herein, the term "isolated," when referring to a nucleic acid or polypeptide refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the body, including (1) the purification from other naturally-occurring associated structures or  
10 compounds, or (2) the association with structures or compounds to which it is not normally associated in the body are within the meaning of "isolated" as used herein. The nucleic acids or polypeptides described herein may be isolated or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the  
15 art.

As used herein, the terms "amplifying" and "amplification" refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (e.g., specific degenerate oligonucleotide  
20 primer pairs) for amplifying (e.g., by polymerase chain reaction, PCR) naturally expressed (e.g., genomic or mRNA) or recombinant (e.g., cDNA) nucleic acids of the invention (e.g., target-binding sequences of the invention) *in vivo* or *in vitro*.

The term "7- transmembrane receptor" means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma  
25 membrane seven times (thus, the seven domains are called "transmembrane" or "TM" domains TM I to TM VII). The families of olfactory and certain taste receptors each belong to this super-family. 7-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

30 The term "library" means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated chemosensory, particularly olfactory receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of

vectors that incorporate the amplified ligand-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding an olfactory receptor.

5 The term "nucleic acid" or "nucleic acid sequence" refers to a deoxy-  
ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded  
form. The term encompasses nucleic acids, i.e., oligonucleotides, containing known  
analogues of natural nucleotides. The term also encompasses nucleic-acid-like  
structures with synthetic backbones (see e.g., *Oligonucleotides and Analogues, a*  
*Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Antisense Strategies,*  
*Annals of the N.Y. Acad. of Sci.*, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan  
10 *J. Med. Chem.* 36:1923-1937 (1993); *Antisense Research and Applications* (1993,  
CRC Press), WO 97/03211; WO 96/39154; Mata, *Toxicol. Appl. Pharmacol.*  
144:189-197 (1997); Strauss-Soukup, *Biochemistry* 36:8692-8698 (1997); Samstag,  
*Antisense Nucleic Acid Drug Dev.*, 6:153-156 (1996)).

15 Unless otherwise indicated, a particular nucleic acid sequence also implicitly  
encompasses conservatively modified variants thereof (e.g., degenerate codon  
substitutions) and complementary sequences, as well as the sequence explicitly  
indicated. Specifically, degenerate codon substitutions may be achieved by  
generating, e.g., sequences in which the third position of one or more selected codons  
is substituted with mixed-base and/or deoxyinosine residues (Batzner *et al.*, *Nucleic*  
20 *Acid Res.*, 19:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.*, 260:2605-08 (1985);  
Rossolini *et al.*, *Mol. Cell. Probes*, 8:91-98 (1994)). The term nucleic acid is used  
interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

The terms "polypeptide," "peptide" and "protein" are used interchangeably  
herein to refer to a polymer of amino acid residues. The terms apply to amino acid  
25 polymers in which one or more amino acid residue is an artificial chemical mimetic of  
a corresponding naturally occurring amino acid, as well as to naturally occurring  
amino acid polymers and non-naturally occurring amino acid polymer.

The term "plasma membrane translocation domain" or simply "translocation  
domain" means a polypeptide domain that, when incorporated into the amino terminus  
30 of a polypeptide coding sequence, can with great efficiency "chaperone" or  
"translocate" the hybrid ("fusion") protein to the cell plasma membrane. For instance,  
a "translocation domain" may be derived from the amino terminus of the bovine  
rhodopsin receptor polypeptide. In one embodiment, the translocation domain may be

functionally equivalent to an exemplary translocation domain (5'-MNGTEGPNFYVPFSNKTGVV; SEQ ID NO: 518). However, rhodopsin from any mammal may be used, as can other translocation facilitating sequences. Thus, the translocation domain is particularly efficient in translocating 7-transmembrane fusion proteins to the plasma membrane, and a protein (e.g., an olfactory receptor polypeptide) comprising an amino terminal translocating domain will be transported to the plasma membrane more efficiently than without the domain. However, if the N-terminal domain of the polypeptide is active in binding, the use of other translocation domains may be preferred.

“Functional equivalency” means the domain’s ability and efficiency in translocating newly translated proteins to the plasma membrane as efficiently as exemplary SEQ ID NO: 518 under similar conditions; relatively efficiencies are measured (in quantitative terms) and compared, as described herein. Domains falling within the scope of the invention can be determined by routine screening for their efficiency in translocating newly synthesized polypeptides to the plasma membrane in a cell (mammalian, *Xenopus*, and the like) with the same efficiency as the twenty amino acid long translocation domain SEQ ID NO: 518, as described in detail below.

The “translocation domain,” “ligand-binding domain,” and chimeric receptors compositions described herein also include “analogs,” or “conservative variants” and “mimetics” (“peptidomimetics”) with structures and activity that substantially correspond to the exemplary sequences. Thus, the terms “conservative variant” or “analog” or “mimetic” refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the polypeptide’s (the conservative variant’s) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (e.g., acidic, basic, positively or negatively charged, polar or non-polar, *etc.*) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity. Conservative substitution tables providing functionally similar amino acids are well known in the art.

More particularly, “conservatively modified variants” applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences,

conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids

5 encode any given protein.

For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide.

10 Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only

15 codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

Conservative substitution tables providing functionally similar amino acids are well known in the art. For example, one exemplary guideline to select conservative substitutions includes (original residue followed by exemplary substitution): ala/gly or

20 ser; arg/lys; asn/gln or his; asp/glu; cys/ser; gln/asn; gly/asp; gly/ala or pro; his/asn or gln; ile/leu or val; leu/ile or val; lys/arg or gln or glu; met/leu or tyr or ile; phe/met or leu or tyr; ser/thr; thr/ser; trp/tyr; tyr/trp or phe; val/ile or leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that

25 are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g., Creighton, Proteins*, W.H. Freeman and Company (1984); Schultz and Schimer, *Principles of Protein Structure*, Springer-Verlag (1979)). One of skill in the art will appreciate that the above-identified substitutions are not the only possible conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In



addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, e.g., translocation domains, ligand-binding domains, or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or may be a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity.

As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the invention, i.e., that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, i.e., to induce or stabilize a secondary structure, e.g., a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, e.g., glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, e.g., ketomethylene (e.g.,  $-C(=O)-CH_2-$  for  $-C(=O)-NH-$ ), aminomethylene ( $CH_2-NH$ ), ethylene, olefin ( $CH=CH$ ), ether ( $CH_2-O$ ), thioether ( $CH_2-S$ ), tetrazole ( $CN_4$ ), thiazole, retroamide, thioamide, or ester (see, e.g., Spatola, *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, 7:267-357, "Peptide Backbone Modifications," Marcel Dekker, NY (1983)). A polypeptide can also be characterized as a mimetic by

containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include  $^{32}\text{P}$ , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are optionally directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one

source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

5 A "promoter" is defined as an array of nucleic acid sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter  
10 that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the  
15 expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (e.g., "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other  
20 biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, e.g., inducible or constitutive expression of a fusion protein comprising a translocation domain of the  
25 invention and a nucleic acid sequence amplified using a primer of the invention.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

30 The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acid, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer

sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology - Hybridisation with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent

5 conditions are selected to be about 5-10° C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength pH. The  $T_m$  is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at  $T_m$ , 50% of the probes are occupied at

10 equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the

15 addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, optionally 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1 % SDS at 65°C. Such

20 hybridizations and wash steps can be carried out for, e.g., 1, 2, 5, 10, 15, 30, 60; or more minutes.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially related if the polypeptides that they encode are substantially related. This occurs, for example, when a copy of a nucleic acid is created using the maximum

25 codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1x SSC at 45°C. Such hybridizations and wash steps can be carried out for, e.g., 1, 2, 5, 10, 15, 30, 60, or

30 more minutes. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad  
5 immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair  
10 having one “light” (about 25 kDa) and one “heavy” chain (about 50-70 kDa). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these light and heavy chains respectively.

A “chimeric antibody” is an antibody molecule in which (a) the constant  
15 region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.*, an enzyme, toxin, hormone, growth factor, drug, *etc.*; or (b) the variable region, or a portion thereof, is altered, replaced or  
20 exchanged with a variable region having a different or altered antigen specificity.

An “anti-OR” antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by a OR gene, cDNA, or a subsequence thereof.

The term “immunoassay” is an assay that uses an antibody to specifically bind an antigen. The immunoassay is characterized by the use of specific binding  
25 properties of a particular antibody to isolate, target, and/or quantify the antigen.

The phrase “specifically (or selectively) binds” to an antibody or, “specifically (or selectively) immunoreactive with,” when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated  
30 immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and do not substantially bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular

protein. For example, polyclonal antibodies raised to an OR family member from specific species such as rat, mouse, or human can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the OR polypeptide or an immunogenic portion thereof and not with other proteins, except for orthologs or polymorphic variants and alleles of the OR polypeptide. This selection may be achieved by subtracting out antibodies that cross-react with OR molecules from other species or other OR molecules. Antibodies can also be selected that recognize only OR GPCR family members but not GPCRs from other families. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (*see, e.g., Harlow & Lane, Antibodies, A Laboratory Manual, (1988), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity*). Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

The phrase "selectively associates with" refers to the ability of a nucleic acid to "selectively hybridize" with another as defined above, or the ability of an antibody to "selectively (or specifically) bind to a protein, as defined above.

The term "expression vector" refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, i.e., drive only transient expression in a cell. The term includes recombinant expression "cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

By "host cell" is meant a cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, HEK-293, and the like, *e.g.,* cultured cells, explants, and cells *in vivo*.

### C. Isolation and Expression of Olfactory Receptors

Isolation and expression of the ORs, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand-binding regions and libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of the genes and nucleic acids (e.g., promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, e.g., bacterial, yeast, insect or plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, e.g., Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature.

See, e.g., Sambrook, ed., *Molecular Cloning: a Laboratory manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I*,  
5 Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, e.g., analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid  
10 chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, e.g., fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (e.g., SDS-  
15 PAGE), RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned  
20 or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (PCR Protocols, a Guide to Methods and Applications, ed. Innis. Academic Press, N.Y.  
25 (1990) and PCR Strategies, ed. Innis, Academic Press, Inc., N.Y. (1995), ligase chain reaction (LCR) (see, e.g., Wu, *Genomics* 4:560 (1989); Landegren, *Science* 241:1077,(1988); Barringer, *Gene* 89:117 (1990)); transcription amplification (see, e.g., Kwok, *PNAS*, 86:1173 (1989)); and, self-sustained sequence replication (see, e.g., Guatelli, *PNAS*, 87:1874 (1990)); Q Beta replicase amplification (see, e.g.,  
30 Smith, *J. Clin. Microbiol.* 35:1477-1491 (1997)); automated Q-beta replicase amplification assay (see, e.g., Burg, *Mol. Cell. Probes* 10:257-271 (1996)) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger, *Methods Enzymol.* 152:307-316 (1987); Sambrook;



Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563-564 (1995).

Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, *e.g.*, U.S. Pat. No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that, when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the ligand-binding region coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted ligand-binding domain comprises substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify ligand-binding regions of olfactory receptor proteins. These domain regions may vary for different ligands, and more particularly odorants; thus, what may be a minimal binding region for one ligand, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane OR.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL3' (SEQ ID NO: 519). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII).

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI 3' (SEQ ID NO: 520) (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)I(AT)(C/T)GT-3' (SEQ ID NO: 521)). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL (SEQ ID NO: 522), encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CANGT-3' (SEQ ID NO: 522). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) (SEQ ID NO: 523) strategy computer program is accessible as <http://blocks.fhcr.org/codehop.html>, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (see, e.g., Rose, *Nucleic Acids Res.* 26:1628-1635 (1998); Singh, *Biotechniques*, 24:318-19 (1998)).

Means to synthesize oligonucleotide primer pairs are well known in the art. "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition. Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g., Hoops, Nucleic Acids Res.* 25:4866-4871 (1997). Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g., Morales, Nat. Struct. Biol.* 5:950-954 (1998)). For example, two degenerate bases can be the pyrimidine base 6H, 8H, 3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g., Hill, PNAS*, 95:4258-63 (1998)). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine, 3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, *see above*). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 524) and  
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 525).
- (b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 526); and  
5'-GGGGCTGCAGACACC(AC/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 527)
- (c) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)GG-3' (SEQ ID NO: 528) and  
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 558)

Nucleic acids that encode ligand-binding regions of olfactory receptors may be generated by amplification (*e.g., PCR*) of appropriate nucleic acid sequences using

degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, e.g., olfactory neurons or olfactory epithelium.

Isolation from olfactory receptor-expressing cells is well known in the art (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (see, e.g., Buiakova, *PNAS*, 93:9858-63 (1996)). Shirley, *Eur. J. Biochem.* 32:485-494 (1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211-216 (1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, e.g., antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260-8270 (1999), describes differentiated olfactory receptor-expressing cells in culture that respond to odorants, as measured by an influx of calcium.

In one embodiment, hybrid protein-coding sequences comprising nucleic acids ORs fused to the translocation sequences described herein may be constructed. Also provided are hybrid ORs comprising the translocation motifs and ligand-binding domains of olfactory receptors. These nucleic acid sequences can be operably linked to transcriptional or translational control elements, e.g., transcription and translation initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can also be used to express the fusion polypeptide receptor, including, e.g., a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and

distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227-236 (1998)). Receptor genes are normally expressed in a small subset of neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

In another embodiment, fusion proteins, either having C-terminal or, more preferably, N-terminal translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional elements for, e.g., protein detection, purification, or other applications. Detection and purification facilitating domains include, e.g., metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g., Ottavi, Biochimie* 80:289-293 (1998)), subtilisin protease recognition motif (*see, e.g., Polyak, Protein Eng.* 10:615-619 (1997)); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a polypeptide-encoding nucleic acid sequence linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g., Williams, Biochemistry* 34:1787-1797 (1995)), and an amino terminal translocation domain. The histidine residues facilitate detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature (*see, e.g., Kroll, DNA Cell. Biol.* 12:441-53 (1993)).

Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent

literature (see, e.g., Roberts, *Nature* 328:731 (1987); Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10 (1995); Sambrook; Tijssen; Ausubel). Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (e.g., episomal expression systems). Selection markers can be incorporated into expression cassettes and vectors to confer a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (e.g., chloramphenicol, kanamycin, G418, bleomycin, hygromycin) or herbicide resistance (e.g., chlorosulfuron or Basta) to permit selection of those cells transformed with the desired DNA sequences (see, e.g., Blondelet-Rouault, *Gene* 190:315-17 (1997); Aubrecht, *J. Pharmacol. Exp. Ther.*, 281:992-97 (1997)). Because selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

A chimeric nucleic acid sequence may encode a ligand-binding domain within any 7-transmembrane polypeptide. 7-transmembrane receptors belong to a superfamily of transmembrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-transmembrane receptor polypeptides have similar primary sequences and secondary and tertiary structures, structural domains (e.g., TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that characterize profiles of the hydrophobicity and variability of analyzed sequences. To predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969-977 (1999); Rost, *Protein Sci.* 4:521-533 (1995). Periodicity detection enhancement and alpha

helical periodicity index can be done as by, *e.g.*, Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, *see, e.g.*, Peitsch, *Receptors Channels* 4:161-164 (1996); Cronet, *Protein Eng.* 6:59-64 (1993) (homology and "discover modeling"); <http://bioinfo.weizmann.ac.il/>.

5       The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, *e.g.*, TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (*e.g.*, PCR) from mRNA of or cDNA derived from, *e.g.*, olfactory receptor-expressing neurons or genomic DNA.

Libraries of olfactory receptor ligand-binding TM domain sequences can  
10       include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the seven domains can be identified by various analyses well known in the art, including, *e.g.*, homology modeling, Fourier analysis and helical periodicity (*see, e.g.*, Pilpel  
15       *supra*), as described above. Using this information sequences flanking the seven domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of,  
20       for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the olfactory receptors described herein, coupled to additional amino acids representing all or part of another  
25       G protein receptor, preferably a member of the 7TM superfamily. These chimeras can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the seven transmembrane protein described herein, and the  
30       remaining portion or portions come from another G protein-coupled receptor. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled

in the art can readily be used to create such chimeric receptors. The use of such chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous GPCR extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, *e.g.*, green fluorescent protein,  $\beta$ -gal, glutamate receptor, and the rhodopsin presequence.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to an olfactory receptor disclosed herein can be isolated using the nucleic acid probes described above. It is hypothesized that allelic differences in receptors may explain why there is a difference in olfactory sensation in different human subjects. Accordingly, the identification of such alleles may be significant, especially with respect to producing receptor libraries that adequately represent the olfactory capability of the human population, *i.e.*, which take into account allelic differences in different individuals. Alternatively, expression libraries can be used to clone olfactory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against an olfactory polypeptide, which also recognize and selectively bind to the olfactory receptor homolog.

Also within the scope of the invention are host cells for expressing the ORs, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the olfactory receptors, fragments, or variants of the invention, one of skill typically subclones the nucleic acid sequence of interest into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable



bacterial promoters are well known in the art and described, *e.g.*, in Sambrook *et al.* However, bacterial or eukaryotic expression systems can be used.

Any of the well-known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Sambrook *et al.*) It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g.*, WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

#### **D. Immunological Detection of OR Polypeptides**

In addition to the detection of OR genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect ORs, *e.g.*, to identify olfactory receptor cells, and variants of OR family members. Immunoassays can be used to qualitatively or quantitatively analyze the ORs. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

##### **1. Antibodies to OR family members**

Methods of producing polyclonal and monoclonal antibodies that react specifically with a OR family member are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *supra*; Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986); and Kohler & Milstein, *Nature*, 256:495-97 (1975)). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by

immunizing rabbits or mice (*see, e.g., Huse et al., Science, 246:1275-81 (1989); Ward et al., Nature, 341:544-46 (1989)*)).

A number of OR-comprising immunogens may be used to produce antibodies specifically reactive with a OR family member. For example, a recombinant OR protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, *e.g.*, the conserved motifs that are used to identify members of the OR family. Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen. Naturally occurring protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in the art. For example, an inbred strain of mice (*e.g.*, BALB/C mice) or rabbits may be immunized with the protein using a standard adjuvant, such as Freund's adjuvant, and a standard immunization protocol. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the OR. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (*see Harlow & Lane, supra*).

Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen may be immortalized, commonly by fusion with a myeloma cell (*see Kohler & Milstein, Eur. J. Immunol., 6:511-19 (1976)*)). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a

vertebrate host. Alternatively, one may isolate DNA sequences which encode a monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275-1281 (1989).

5 Monoclonal antibodies and polyclonal sera are collected and titrated against the immunogen protein in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Typically, polyclonal antisera with a titer of 109 or greater are selected and tested for their cross reactivity against non-OR proteins, or even other OR family members or other related proteins from other  
10 organisms, using a competitive binding immunoassay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a Kd of at least about 0.1 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

Once OR family member specific antibodies are available, individual OR  
15 proteins can be detected by a variety of immunoassay methods. For a review of immunological and immunoassay procedures, see *Basic and Clinical Immunology* (Stites & Terr eds., 7th ed. 1991). Moreover, the immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in Enzyme Immunoassay (Maggio, ed., 1980); and Harlow & Lane, *supra*.

## 20 **2. Immunological binding assays**

OR proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (see, e.g., U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, see also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993);  
25 *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed. 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case an OR family member or an antigenic subsequence thereof). The antibody (e.g., anti-OR) may be produced by any of a number of means well known to those of skill in the art and as described above.

30 Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent may be a labeled OR polypeptide or a labeled anti-OR antibody. Alternatively, the

labeling agent may be a third moiety, such as a secondary antibody that specifically binds to the antibody/OR complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see, e.g., Kronval et al., J. Immunol., 111:1401-1406 (1973); Akerstrom et al., J. Immunol., 135:2589-2542 (1985)*). The labeling agent can be modified with a detectable moiety, such as biotin, to which another molecule can specifically bind, such as streptavidin.

10 A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

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**a. Non-competitive assay formats**

Immunoassays for detecting an OR protein in a sample may be either competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of antigen is directly measured. In one preferred "sandwich" assay, for example, the anti-OR antibodies can be bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the OR protein present in the test sample. The OR protein is thus immobilized is then bound by a labeling agent, such as a second OR antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g., streptavidin*, to provide a detectable moiety.

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**b. Competitive assay formats**

In competitive assays, the amount of OR protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) OR

protein displaced (competed away) from an anti-OR antibody by the unknown OR protein present in a sample. In one competitive assay, a known amount of OR protein is added to a sample and the sample is then contacted with an antibody that specifically binds to the OR. The amount of exogenous OR protein bound to the antibody is inversely proportional to the concentration of OR protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of OR protein bound to the antibody may be determined either by measuring the amount of OR protein present in a OR/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of OR protein may be detected by providing a labeled OR molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known OR protein is immobilized on a solid substrate. A known amount of anti-OR antibody is added to the sample, and the sample is then contacted with the immobilized OR. The amount of anti-OR antibody bound to the known immobilized OR protein is inversely proportional to the amount of OR protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. **Cross-reactivity determinations**

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, OR proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the OR polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percent cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related

homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the OR family can be used in cross-reactivity determinations.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a OR family member, to the immunogen protein (*i.e.*, OR protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to specifically bind to the polyclonal antibodies generated to a OR immunogen.

Antibodies raised against OR conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the OR family, but not to GPCRs from other families.

Polyclonal antibodies that specifically bind to a particular member of the OR family, *e.g.*, AOLFR1, can be make by subtracting out cross-reactive antibodies using other OR family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human AOLFR1 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OR1 or mouse OR1.

#### **d. Other assay formats**

Western blot (immunoblot) analysis is used to detect and quantify the presence of OR protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind the OR protein. The anti-OR polypeptide antibodies specifically bind to the OR polypeptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-OR antibodies.

Other, assay formats include liposome immunoassays (LIA), which use liposomes designed to bind specific molecules (e.g., antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (see Monroe *et al.*, *Amer. Clin. Prod. Rev.*, 5:34-41 (1986)).

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**e. Reduction of non-specific binding**

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

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**f. Labels**

The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, most any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (e.g., DYNABEADS<sup>TM</sup>) (SEQ ID NO: 529), fluorescent dyes (e.g., fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (e.g., <sup>3</sup>H, <sup>125</sup>I, <sup>35</sup>S, <sup>14</sup>C, or <sup>32</sup>P), enzymes (e.g., horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (e.g., polystyrene, polypropylene, latex, *etc.*).

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The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

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Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to another molecules (*e.g.*, streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a OR protein, or secondary antibodies that recognize anti-OR.

The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, *etc.* Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems that may be used, *see* U.S. Patent No. 4,391,904.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, by means of photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.



### **E. Detection of Olfactory Modulators**

Methods and compositions for determining whether a test compound specifically binds to a mammalian chemosensory, and more particularly, an olfactory receptor of the invention, both *in vitro* and *in vivo* are described below. Many aspects of cell physiology can be monitored to assess the effect of ligand-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory neurons. These receptors bind odorants and initiate the transduction of chemical stimuli into electrical signals. An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. Some examples include the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The OR protein of the assay will typically be selected from a polypeptide having a sequence selected from SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID.

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 25 ID. NO. 327, SEQ. ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID.  
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NO. 403, SEQ. ID. NO. 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413, SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ. ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ. ID. NO. 495, SEQ. ID. NO. 497, SEQ. ID. NO. 499, SEQ. ID. NO. 501, SEQ. ID. NO. 503, SEQ. ID. NO. 505, SEQ. ID. NO. 507, SEQ. ID. NO. 509 and SEQ. ID. NO. 511, or conservatively modified variant thereof.

Alternatively, the OR protein of the assay can be derived from a eukaryote host cell and can include an amino acid subsequence having at least about 30-40% amino acid sequence identity to SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID.

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ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

Preferably, the amino acid sequence identity will be at least 50-75% preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of an OR protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand-binding domain, subunit association domain, active site, and the like. Either the OR protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein. As discussed *infra*, the family of ORs provided herein exhibits substantial sequence similarity at both the DNA and protein level, but also significant dissimilarity. In particular, the members possess an average percentage sequence identity to other members of the family when determined over the full length of the gene by about 30%. Moreover, different members of the genes at the protein level exhibit an average on the order of about 40% sequence identity to other members of the family when the full length protein sequences are compared. However, while there exist differences, there are characteristic similarities, *e.g.* the consensus sequence already mentioned, which further define members of this novel genus of receptors.

Modulators of OR activity can be tested using OR polypeptides as described above, either recombinant or naturally occurring. The protein can be isolated, expressed in a cell, expressed in a membrane derived from a cell, expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

## 1. In vitro binding assays

Olfactory transduction can also be examined *in vitro* with soluble or solid state reactions, using a full-length OR or a chimeric molecule such as an extracellular domain or transmembrane region, or combination thereof, of a OR covalently linked to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of an OR. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises all or part of a OR polypeptide, as well an additional sequence that facilitates the localization of the OR to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein, *e.g.* bovine or another mammalian rhodopsin.

Ligand binding to a OR protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid monolayer, or in vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties.

Receptor-G protein interactions can also be examined. For example, binding of the G protein to the receptor or its release from the receptor can be examined. For example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation.

An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins.

Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

In another embodiment of the invention, a GTP $\gamma$ S assay may be used. As described above, upon activation of a GPCR, the G $\alpha$  subunit of the G protein complex is stimulated to exchange bound GDP for GTP. Ligand-mediated stimulation of G protein exchange activity can be measured in a biochemical assay measuring the binding of added radioactively-labeled GTP $\gamma$ <sup>35</sup>S to the G protein in the presence of a putative ligand. Typically, membranes containing the chemosensory receptor of interest are mixed with a complex of G proteins. Potential inhibitors and/or activators and GTP $\gamma$ S are added to the assay, and binding of GTP $\gamma$ S to the G protein is measured. Binding can be measured by liquid scintillation counting or by any other means known in the art, including scintillation proximity assays (SPA). In other assays formats, fluorescently-labeled GTP $\gamma$ S can be utilized.

## 2. Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor odorant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the olfactory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nanoseconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the

polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the olfactory receptors of the invention, fluorescence-labeled odorants or auto-fluorescent odorants may be used.

Fluorescence polarization ( $P$ ) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

Where  $\parallel$  is the intensity of the emission light parallel to the excitation light plane and  $\perp$  is the intensity of the emission light perpendicular to the excitation light plane.  $P$ , being a ratio of light intensities, is a dimensionless number. For example, the Beacon® and Beacon 2000™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley, M. E. (1991) in Journal of Analytical Toxicology, pp. 236-240, which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity ( $\eta$ ), absolute temperature ( $T$ ), molecular volume ( $V$ ), and the gas constant ( $R$ ) by the following equation:

$$Rotational\ Relaxation\ Time = \frac{3\eta V}{RT}$$

The rotational relaxation time is small ( $\approx 1$  nanosecond) for small molecules (e.g. fluorescein) and large ( $\approx 100$  nanoseconds) for large molecules (e.g. immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been



used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

### 3. Solid state and soluble high throughput assays

5 In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc.; a domain that is covalently linked to a heterologous  
10 protein to create a chimeric molecule; an OR protein; or a cell or tissue expressing an OR protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based in vitro assays in a high throughput format, where the domain, chimeric molecule, OR protein, or cell or tissue expressing the OR is attached to a solid phase substrate.

15 In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate  
20 can assay about 100 (*e.g.*, 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is also possible to assay multiple compounds in each plate well. Further, it is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More  
25 recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, *e.g.*, via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is  
30 fixed to a solid support, and the tagged molecule of interest (*e.g.*, the olfactory transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural

binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors, immunoglobulin receptors and antibodies, the cadherein family, the integrin family, the selectin family, and the like; *see, e.g.*, Pigott & Power, The Adhesion Molecule Facts Book I (1993)). Similarly, toxins and venoms, viral epitopes, hormones (*e.g.*, opiates, steroids, *etc.*), intracellular receptors (*e.g.*, which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D; peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes, polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about 5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethylene glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulphydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent that fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups that are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. See, e.g., Merrifield, *J. Am. Chem. Soc.*, 85:2149-54 (1963) (describing solid phase synthesis of, e.g., peptides); Geysen *et al.*, *J. Immun. Meth.*, 102:259-74 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron*, 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al.*, *Science*, 251:767-77 (1991); Sheldon *et al.*, *Clinical Chemistry*, 39(4):718-19 (1993); and Kozal *et al.*, *Nature Medicine*, 2(7):753759 (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

#### 4. Computer-based assays

Yet another assay for compounds that modulate OR protein activity involves computer assisted compound design, in which a computer system is used to generate a three-dimensional structure of an OR protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the protein structure are then examined to identify regions of the structure that have the ability to bind, e.g., ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a OR polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID

NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID  
NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID  
NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID  
NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID  
5 NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID  
NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID  
NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID  
NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID  
NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,  
10 SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID  
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,  
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID  
NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,  
SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID  
15 NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,  
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID  
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,  
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID  
NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,  
20 SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID  
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,  
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID  
NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,  
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID  
25 NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,  
SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID  
NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,  
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID  
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,  
30 SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID  
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,  
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NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, 5 SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID 10 NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, 15 SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID 20 NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, and conservatively modified versions thereof.

The amino acid sequence represents the primary sequence or subsequence of the protein, which encodes the structural information of the protein. At least 10 25 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino acids) are entered into the computer system from computer keyboards, computer readable substrates that include, but are not limited to, electronic storage media (*e.g.*, magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM), information distributed by internet sites, and by RAM. The three-dimensional 30 structural model of the protein is then generated by the interaction of the amino acid sequence and the computer system, using software known to those of skill in the art. .

The amino acid sequence represents a primary structure that encodes the information necessary to form the secondary, tertiary and quaternary structure of the

protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as "energy terms," and primarily include electrostatic potentials, hydrophobic potentials, solvent accessible surfaces, and hydrogen bonding. Secondary energy terms include van der  
5 Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

The tertiary structure of the protein encoded by the secondary structure is then  
10 formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the  
15 computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand-binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of  
20 compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the OR protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of OR genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related  
25 technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used  
30 to identify patients having such mutated genes. Identification of the mutated OR genes involves receiving input of a first nucleic acid or amino acid sequence of a OR gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is

- then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once the first and second sequences are compared, nucleotide or amino acid differences between the sequences are identified.
- 5 Such sequences can represent allelic differences in various OR genes, and mutations associated with disease states and genetic traits.

### 5. Cell-based binding assays

- In a preferred embodiment, an OR polypeptide is expressed in a eukaryotic cell as a chimeric receptor with a heterologous, chaperone sequence that facilitates its maturation and targeting through the secretory pathway. In a preferred embodiment, the heterologous sequence is a rhodopsin sequence, such as an N-terminal fragment of a rhodopsin. Such chimeric OR receptors can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a functional G protein, *e.g.*, G $\alpha$ 15, that is capable of coupling the chimeric receptor to an intracellular signaling pathway or to a signaling protein such as phospholipase C. Activation of such chimeric receptors in such cells can be detected using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell.
- 15

- Activated GPCR receptors become substrates for kinases that phosphorylate the C-terminal tail of the receptor (and possibly other sites as well). Thus, activators will promote the transfer of  $^{32}\text{P}$  from gamma-labeled GTP to the receptor, which can be assayed with a scintillation counter. The phosphorylation of the C-terminal tail will promote the binding of arrestin-like proteins and will interfere with the binding of G proteins. The kinase/arrestin pathway plays a key role in the desensitization of many GPCR receptors. For example, compounds that modulate the duration an olfactory receptor stays active would be useful as a means of prolonging a desired odor or cutting off an unpleasant one. For a general review of GPCR signal transduction and methods of assaying signal transduction, *see, e.g., Methods in Enzymology*, vols. 237 and 238 (1994) and volume 96 (1983); Bourne *et al.*, *Nature*, 10:349:117-27 (1991); Bourne *et al.*, *Nature*, 348:125-32 (1990); Pitcher *et al.*, *Annu. Rev. Biochem.*, 67:653-92 (1998).
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- 30

OR modulation may be assayed by comparing the response of an OR polypeptide treated with a putative OR modulator to the response of an untreated

control sample. Such putative OR modulators can include odorants that either inhibit or activate OR polypeptide activity. In one embodiment, control samples (untreated with activators or inhibitors) are assigned a relative OR activity value of 100. Inhibition of an OR polypeptide is achieved when the OR activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of an OR polypeptide is achieved when the OR activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (*i.e.*, electrical potential) of the cell or membrane expressing a OR protein. One means to determine changes in cellular polarization is by measuring changes in current (thereby measuring changes in polarization) with voltage-clamp and patch-clamp techniques, *e.g.*, the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575-1595 (1997)). Whole cell currents are conveniently determined using the standard. Other known assays include: radiolabeled ion flux assays and fluorescence assays using voltage-sensitive dyes (*see, e.g.*, Vestergaard-Bogind *et al.*, *J. Membrane Biol.*, 88:67-75 (1988); Gonzales & Tsien, *Chem. Biol.*, 4:269277 (1997); Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185-193 (1991); Holevinsky *et al.*, *J. Membrane Biology*, 137:59-70 (1994)). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as  $Ca^{2+}$ , IP3, cGMP, or cAMP.

Preferred assays for GPCRs include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G protein coupled receptors as negative or positive controls to assess activity of tested compounds. In



assays for identifying modulatory compounds (*e.g.*, agonists, antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed  
5 in the Molecular Probes 1997 Catalog. For G protein coupled receptors, promiscuous G proteins such as  $G\alpha 15$  and  $G\alpha 16$  can be used in the assay of choice (Wilkie *et al.*, *PNAS*, 88:10049-53 (1991)). Such promiscuous G proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*,  
10 increases in second messengers such as IP<sub>3</sub>, which releases intracellular stores of calcium ions. Activation of some G protein coupled receptors stimulates the formation of inositol triphosphate (IP<sub>3</sub>) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature*, 312:315-21 (1984)). IP<sub>3</sub> in turn stimulates the release of intracellular calcium ion stores. Thus, a change in  
15 cytoplasmic calcium ion levels, or a change in second messenger levels such as IP<sub>3</sub> can be used to assess G protein coupled receptor function. Cells expressing such G protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in  
20 calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are  
25 cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (*see, e.g.*, Altenhofen *et al.*, *PNAS*, 88:9868-72 (1991) and Dhalla *et al.*, *Nature*, 347:184-187 (1990)). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents  
30 that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-gated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*,

certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors, serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, OR protein activity is measured by expressing a  
5 OR gene in a heterologous cell with a promiscuous G protein that links the receptor to a phospholipase C signal transduction pathway (*see* Offermanns & Simon, *J. Biol. Chem.*, 270:15175-15180 (1995)). Optionally the cell line is HEK-293 (which does not naturally express OR genes) and the promiscuous G protein is G $\alpha$ 15/G $\alpha$ 16 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by  
10 measuring changes in intracellular Ca<sup>2+</sup> levels, which change in response to modulation of the OR signal transduction pathway via administration of a molecule that associates with a OR protein. Changes in Ca<sup>2+</sup> levels are optionally measured using fluorescent Ca<sup>2+</sup> indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be  
15 measured using immunoassays. The method described in Offermanns & Simon, *J. Bio. Chem.*, 270:15175-15180 (1995), may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159-164 (1994), may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent 4,115,538, herein  
20 incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled  
25 cells are treated with a test compound for one hour. The treated cells are lysed and extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the  
30 presence of buffer control (which may or may not contain an agonist).

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing an OR protein of interest is contacted with a test compound for a sufficient time to effect any

interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent 5,436,128, herein incorporated by reference. The reporter genes can be, *e.g.*, chloramphenicol acetyltransferase, luciferase, '3-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (*see, e.g.*, Mistili & Spector, *Nature Biotechnology*, 15:961-64 (1997)).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the OR protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the OR protein of interest.

#### **6. Transgenic non-human animals expressing olfactory receptors**

Non-human animals expressing one or more olfactory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand-binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of the translocation domains of the invention in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize odorants/ligands that can bind to a specific or sets of receptors. Such

vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

Means to infect/express the nucleic acids and vectors, either individually or as libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses. When electrodes are located on the olfactory bulb surface it is possible to record stable responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287-291 (1997)). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinates facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of one turbinate bone or were placed in corresponding positions on four turbinate bones and moved together up toward the top of the bone. *See also*, Scott, *J. Neurophysiol.* 77:1950-1962 (1997); Scott, *J. Neurophysiol.* 75:2036-2049 (1996); Ezech, *J. Neurophysiol.* 73:2207-2220 (1995). In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and medial surface of the turbinates (*see, e.g.*, Youngentob, *J. Neurophysiol.* 73:387-398 (1995)). Extracellular potassium activity (aK) measurements can also be carried out *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1-5 (1991)).

The OR sequences of the invention can be for example expressed in animal nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *PNAS*, 96:4040-45 (1999).

The endogenous olfactory receptor genes can remain functional and wild-type (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a "knockout" cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, "gene trap insertion" can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g., Holzschu, Transgenic Res* 6:97-106 (1997)). The insertion of the exogenous is typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene's expression; or a combination thereof. Gene targeting via homologous recombination in pluripotential embryonic stem cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g., see Bijvoet, Hum. Mol. Genet.* 7:53-62 (1998); Moreadith, *J. Mol. Med.* 75:208-216 (1997); Tojo, *Cytotechnology* 19:161-165 (1995); Mudgett, *Methods Mol. Biol.* 48:167-184 (1995); Longo, *Transgenic Res.* 6:321-328 (1997); U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO 93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries of the invention can also be used as reagents to produce "knockout" human cells and their progeny. Likewise, the nucleic acids of the invention can also be used as reagents to produce "knock-ins" in mice. The human or rat OR gene sequences can replace the orthologous ORs in the mouse genome. In this way, a mouse expressing a human or rat OR can be produced. This mouse can then be used to analyze the function of human or rat ORs, and to identify ligands for such ORs.

#### **F. Modulators**

The compounds tested as modulators of an OR family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of an OR gene.

Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to screen large chemical libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

The OR modulating compounds can be used in any number of consumer products, including, but not limited to, perfumes, fragrance compositions, deodorants, air fresheners, foods, drugs, *etc.*, or ingredients thereof, to thereby modulate the odor of the product, composition, or ingredient in a desired manner. As one of skill in the art will recognize, OR modulating compounds can be used to enhance desirable odors, to block malodors, or a combination thereof.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual odorant compositions.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.,* U.S. Patent 5,010,175, Furka, *Int. J. Pept. Prot. Res.*, 37:487-93 (1991) and Houghton *et al.*, *Nature*, 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (*e.g.,* PCT Publication No. WO 91/19735), encoded peptides (*e.g.,* PCT Publication WO 93/20242), random bio-oligomers (*e.g.,* PCT Publication No. WO 92/00091), benzodiazepines (*e.g.,* U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *PNAS*, 90:6909-13 (1993)), vinylous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.*, 114:6568 (1992)), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.*, 114:9217-18 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.*, 116:2661 (1994)), oligocarbamates (Cho *et al.*, *Science*, 261:1303 (1993)), peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.*, 59:658 (1994)), nucleic acid libraries (Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (U.S. Patent 5,539,083), antibody libraries (Vaughn *et al.*, *Nature Biotechnology*, 14(3):309-14 (1996) and PCT/US96/10287), carbohydrate libraries (Liang *et al.*, *Science*, 274:1520-22 (1996) and U.S. Patent 5,593,853), small organic molecule libraries (benzodiazepines, Baum, *C&EN*, Jan 18, page 33 (1993); thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pynrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337; benzodiazepines, 5,288,514, and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.,* 357 MPS, 390 MPS (Advanced Chem Tech, Louisville KY), Symphony (Rainin, Woburn, MA), 433A (Applied Biosystems, Foster City, CA), 9050 Plus (Millipore, Bedford, MA)). In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.,* ComGenex, Princeton, NJ; Tripos, Inc., St. Louis, MO; 3D Pharmaceuticals, Exton, PA; Martek Biosciences; Columbia MD; *etc.*).

**G. Methods for Representing and Predicting the Perception of Odor**

The invention also preferably provides methods for representing the perception of odor (or taste) and/or for predicting the perception of odor (or taste) in a mammal, including in a human. Preferably, such methods may be performed by using the receptors and genes encoding said olfactory receptors disclosed herein.

Also contemplated as within the invention, is a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising: contacting said one or more compounds with the disclosed receptors, preferably wherein the mammal is a human. Also contemplated as within the invention is a method for representing olfactory perception of a particular smell in a mammal, comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  olfactory receptors of said vertebrate, where  $n$  is greater than or equal to 4; and generating from said values a quantitative representation of olfactory perception. The olfactory receptors may be an olfactory receptor disclosed herein, the representation may constitute a point or a volume in  $n$ -dimensional space, may constitute a graph or a spectrum, and may constitute a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced olfactory receptors with a test composition and quantitatively measuring the interaction of said composition with said receptors.

Also contemplated as within the invention, is a method for predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  olfactory receptors of said vertebrate, where  $n$  is greater than or equal to 4, for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  olfactory receptors of said vertebrate, where  $n$  is greater than or equal to 4, for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding



unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal. The olfactory receptors used in this method may include an olfactory receptor disclosed herein.

10 In another embodiment, novel molecules or combinations of molecules are generated which elicit a predetermined olfactory perception in a mammal by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules as described above; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules as described above; comparing the value of olfactory perception in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

20 In another embodiment of the invention, there is provided a method for simulating a fragrance, comprising: for each of a plurality of cloned olfactory receptors, preferably human receptors, ascertaining the extent to which the receptor interacts with the fragrance; and combining a plurality of compounds, each having a previously-ascertained interaction with one or more of the receptors, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an olfactory receptor can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds

substantially stimulate at least 75%, 80% or 90% of the receptors that are substantially stimulated by the fragrance.

In another preferred embodiment of the invention, a plurality of standard compounds are tested against a plurality of olfactory receptors to ascertain the extent to which the receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

#### **H. Kits**

OR genes and their homologs are useful tools for identifying olfactory receptor cells, for forensics and paternity determinations, and for examining olfactory transduction. OR family member-specific reagents that specifically hybridize to OR nucleic acids, such as AOLFR1 probes and primers, and OR family member-specific reagents that specifically bind to an OR protein, *e.g.*, OR antibodies are used to examine olfactory cell expression and olfactory transduction regulation.

Nucleic acid assays for the presence of DNA and RNA for an OR family member in a sample include numerous techniques are known to those skilled in the art, such as southern analysis, northern analysis, dot blots, RNase protection, S1 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such a form so as to be available for hybridization within the cell, while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*, *Biotechniques*, 4:230-50 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, an OR protein can be detected with the various immunoassay

techniques described above. The test sample is typically compared to both a positive control (e.g., a sample expressing a recombinant OR protein) and a negative control.

The present invention also provides for kits for screening for modulators of OR family members. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise any one or more of the following materials: OR nucleic acids or proteins, reaction tubes, and instructions for testing OR activity. Optionally, the kit contains a biologically active OR receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

## EXAMPLES

Genomic, predicted amino acid sequence, and predicted coding sequences (cds), of novel G protein-coupled human odorant receptors, and classes of such receptors, are described. Each example describes a discrete protein and nucleic acid pair. Accordingly, Example 1 describes SEQ. ID. NOS. 1 and 2, for the human olfactory receptor protein designated AOLFR1, and the human DNA encoding AOLFR1, respectively; Example 2 describes SEQ. ID. NOS. 3 and 4, for the human olfactory receptor protein designated AOLFR2, and the human DNA encoding AOLFR2, respectively; and so on in the manner described, through the final Example sequence.

In the protein sequences presented herein, the one-letter code X or Xaa refers to any of the twenty common amino acid residues. In the DNA sequences presented herein, the one letter codes N or n refers to any of the of the four common nucleotide bases, A, T, C, or G.

## EXAMPLES

### **AOLFR1 sequences:**

MKTFSSFLQIGRNMHQGNQTITTEFILLGFFKQDEHQNLLFVFLGMYLVTVIGNGLIIVAIISLD  
TYLHTPMYLFLEANLSFADISSISNSVPKMLVNIQTKSQSISYESCITQMYFSIVFVVIDNLLGTM  
AYDHFVAICHPLNYILMRPRFGILLTVISWELSNIALHTLLQLLFCNHTLPHFFCDLAPLL  
KLSCSDTLINELVLFIVGLSVIIFPFTLSFFSYVCIIRAVLRVSSTQGWKFAFSTCGSHLTVVLFY  
GTIVGVYFFPSSTHPEDTKIGAVLFTVVTPMINPFYISLRNKDMKGALRKILNRKISSL (SEQ ID  
NO: 1)

ATGAAGACTTTTAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAAACCA  
CCATCACTGAATTCATCTCCTGGGATTTTCAAGCAGGATGAGCATCAAAACCTCCTCTTT  
TGCTCTTTCTTGGGTATGTACCTGGTCACTGTGATTGGGAACGGGCTCATCATTTGGGCTA  
TCAGCTGGGATACGACCTTCATACCCCATGTATCTCTTCCTTGCCAATCATCCTTTGCT  
GATATTTCTCCATTTCACACTCAGTCCCAAAATGCTGGTGAATATTCAAACCAAGAGTC

AAATCCATCTCTTATGAGAGCTGCATCACACAGATGTACTTTTCTATTGTGTTTGTGTCATT  
 GACAATTTGCTCTTGGGGACCATGGCCTATGACCACCTTTGTGGCGATCTGCCACCCCTCTGA  
 ATTATACAATTCTCATGCGGGCCAGGTCGGCATTTTGTCTACAGTCATCTCATGGTTCCTC  
 AGTAATATTATTGCTCTGCACACACCCCTTCTGCTCATTCAAATTGCTCTCTGTAAACACAA  
 5 CACTCTCCCACTTCTCTGTGACTTGGCCCTCTGCTCAAACCTGCTGTTCAGATACAT  
 TGATCAATGAGCTTGTGTTGTTATTGTGGGTTTATCAGTTATCATCTTCCCTTTACACTC  
 AGCTCTTTTCTCATGTCTGCATCATCAGAGCTGTCCTGAGAGTATCTCCACACAGGGAA  
 AGTGGAAAGCCTTCTCCACTTGTGGCTCTCACTGCACAGTTGTATTACTGTTCTACGGAAC  
 CATTGTAGGCGTGTACTTTTCCCTCTCCACTCACCTGAGGACATGATAAGATTGGT  
 10 GCTGTCTTCTACTGTGGTGACACCCATGATAAACCCCTTCATCTACAGCTTGAGGAATA  
 AGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTCTTCCCTTGA (SEQ  
 ID NO: 2)

**AOLFR2 sequences:**

15 MMMVLRLNSMEPTFALLGFTDYPKLQIPFLVFLLMYVITVVGNLGMIHIIKINPKFHTPMYFFL  
 SHLSFVDFCYSSIVTPKLLNLVMAKDSIFYFSCMMQYFLSCTAVVTESFLLAVMAYDRFVAIC  
 NPLLYTVAMSQLCALLVAGSYLWGMFPLVLLCYALRLNFGSGPNVINHHFCEYTLAISVSGS  
 DLIPLHLLFSFATVFNEMCTLLIILTSYVFIVTVLKIRSVGRHKAFSTWASHLTATIFHGTILFL  
 YCVPNSKNSRQTVKVASVFYTVVNPMLNPPIYSRLNKDVKDAFWKLIHTQVPPH (SEQ ID NO:  
 20 3)

ATGATGATGGGTTTTAAGGAATCTGAGCATGGAGGCCACCTTTGCCCTTTTAGGTTTACAG  
 ATATCCCAAAGCTTCAGATTCTCTCTCTTCTTGTGTTTCTGCTCATGTATGTTATCACAGTG  
 GTAGGAAACCTTGGGATGATCATAATAATCAAGATTAAACCCCAAATTCACACTCCTATGT  
 25 ACTTTTCTCTAGTCACCTCTCTTTTGTGATTTTGTACTCTTCCATTTGCTCACTCCCAAGC  
 TGTGTGAGAACATTGGTAATGGCAGATAAAAGCATCTTCTACTTACTGCTCATGATGCAGTA  
 CTCTCTGCTCTGCACCTGCTGGTGACAGAGTCTTCTGCTGGCAGTATGGCTCATGAC  
 CGCTTTGTGGCCATCTGCAATCTCTGCTTTATACAGTGGCCATGTACAGAGGCTCTGTG  
 CCGTCTGCTGGTGGCTGGGTCATATCTCTGGGCGCATGTTGGGCCCTTGGTACTCCTTTGTTAT  
 30 GCTCTCCGGTTAAACTCTCTCGGACCTAAATGTAATCAACCCACTCTTTTGTGAGTATACG  
 TCTCATCTCTGTGCTGGCTGTATATACTCATCCCCACCTGCTGCTTTACAGTTCGCCA  
 CCTTCAATGAGATGTGTACACTACTGATCATCTCTCACTTCTATGTTTTCATATTTTGTGACT  
 GTACTAAAAATCCGTCTGTGTAGTGGGCGCCAAAGCCTTCTCCACCTGGGCGCTCCCAAC  
 TGACTGCTATCACCATCTTCCATGGGACCATCTTCTTCTTACTGTGTCACCACTGCCAA  
 35 AACTCTCGGCAACACAGTCAAAGTGGCCTCTGTATTTACACAGTTGTCAACCCCATGCTGA  
 ACCCTCCGATCTACAGCCTAAGGAATAAGACGCTGAAGGATGCTTCTCGGAAGTTAATACA  
 TACACAAGTTCCATTCACTGA (SEQ ID NO: 4)

**AOLFR3 sequences:**

40 MLLTDRNTSGTFTLLGFSDYPELQVPLFLVFLAIYNVTVLGNIGLIIVIKINPKLHTPMYFFLSQ  
 LSFVDFCYSSIIAPKMLVNLVVKDRITSLFCGVVQFFFFCTFVVTESFLLAVMAYDRFVAICNPL  
 LYTVDMSQKLCVLLVVGSYAWGVSCSELTCALKLCFHGFNTINHFCEFSLLSLSCSDTYI  
 NQWLLFFLATNEISTLLIVLTSYAFIVTILKMRSVSGRRKAFSTCASHLTATIFHGTILFLYCV  
 PNSKNSRHTVKVASVFYTVVPMPLNPLIYSRLNKDVKDTVTEILDTKVFYSY (SEQ ID NO: 5)

ATGCTGCTGACAGATAGAAATACAAGTGGGACCACGTTACCCCTCTTGGGCTTCTCAGATT  
 AOCAGAAGCTGCAAGTCCCACTTCTGTTTCTTGGCCATCTACAATGCTCAATGCTGCTCA  
 GGAATATTGGGTTGATTGTGATCATCAAAATCAACCCCAAATGCATACCCCATGTACT  
 TTTTCTCAGCAACTCTCTTTGTGGATTCTGCTATTCTCCATCATTTGCTCCCAAGATG  
 50 TGGTGAACTTGTGTGCAAGACAGAACCAATTCATTTTAGGATGCGTAGTACAAATTTCT  
 TTTTCTCTGTACCTTTGTGGTCACTGAATCTTTTATTAGCTGTGATGGCCTATGACCGC  
 TTGCTGGCCATTTGCAACCCCTGCTCTACACAGTTGACATGCCAGAAACTCTGCGTGC  
 TGCTGGTGTGGGATCCTATGCCTGGGGAGTCTCATGTTCTTGGAACTGACGTGCTCTGC  
 TTTAAAGTTATGTTTCTATGGTTTCAACACAATCAATCACTTCTCTGTGAGTCTCTCCAC  
 55 TACTTCCCTTCTTGCTGTGATACTTACATCAACCAAGTGGCTGCTATTCTTCTTGGCCACC  
 TTTAATGAAATCAGCACACTACTCATGTTCTCACATCTTATGCGTTTCATTGTTGTAACCAT

5 CCTCAAGATGCGTTCACTAGTGGGCGCCGCAAAAGCCTTCTCCACCTGTGCCTCCCACTG  
 ACTGCCATCACCATCTTCCATGGCACCATCCTCTTCCTTTACTGTGTGGCCCAACTCCAAAAA  
 CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCCATGTGTAAT  
 CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC  
 ACCAAAGTCTTCTTACTGA (SEQ ID NO: 6)

**AOLFR4 sequences:**

10 MENQNNVTEFILLGLTENLELWKIFSAVFLVMYVATVLENLLIVVTIITSQSLRSPMYFFLTFLS  
 LLDVMFSSSVVAPKVIVDTLSKSTTISLKGCLTQLFVEHFFGGVGIILLTVMAYDRYVAICKPLHY  
 THMSPRVCLMVGGAWVGFMHAMIQLLFMYQIPFCGNIDHFCIDLFQLLTACTDTHILGL  
 LVTLSNGMMCVAFILILIASYTVILCSLSYSSKGRIHKALSTCSSHLTVVVLFFVPCIFLYMRPV  
 VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

15 ATGGAAAAATCAAAACAATGTGACTGAATTCATCTTCTCTGGGTCTCACAGAGAAGCTGGAGC  
 TGTGGAAAAATATTTCTGCTGTGTTTCTTGTGTCATGTATGTAGCCACAGTGTGGAATACT  
 ACTTATTGTGGTAACATATTATCACAAAGTCAGAGTCTGAGGTACCACTATGTTATTTTCTTA  
 CCTCTTGTGCCCTTTTGGATGTCATGTTCTCATCTGTCGTGCCCCAAGGTGATTTGTAGAC  
 ACCCTCTCCAAGACACATACCATCTCTCTCAAAGGCTGCCTACCCAGCTGTTTGTGGAGC  
 ATTTCTTTGGTGGTGTGGGGATCATCTCTCACTGTATGGCCTATGACCGCTACGTGGC  
 CATCTGTAAGCCCTGCATCACAGCATCATGTAGTCCACGGGTGTGTCGCTAATGGTA  
 GGAGGGGCTTGGGTGGGGGATTATGACGCAATGATACAACCTTCTCTCATGTATCAAA  
 TACCTTCTGTGGTCCTAATATCATAGATCACTTTATGTGATTTGTTTCAGTTGTGTGAC  
 CTGCGCTGCAGGACACCCACATCTGCGGCTCTTAGTTACCTCAACAGTGGGATGATGCT  
 GTGTGGCCATCTTCTTATCTTAATGCGTCTACACGGTCATCTATGTCTCCCTGAAGTCT  
 25 TACAGCTCTAAAGGGCGGCACAAAGCCCTCTCTACCTGCACTCCCACTCACGGTGGTG  
 TATTGTCTTTGTCCCTGTATTTCTTGTGATCATGAGGCGTGTGGTCACTACCCCATAGAC  
 AAGGCAATGGCTGTGTGACAGTCAATCATCACACCACTGTTAAATCCCTGTATCATACAC  
 TGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAACTCTGGATGAAATGGGAGGCTTGG  
 CTGGGAAATAA (SEQ ID NO: 8)

30

**AOLFR5 sequences:**

35 MGKENCTTVAEFILLGLSDVPELTVCLFLLFLLYGVTLANLGMIALIQVSSRLHTPMYFFLSH  
 LSSVDFCYSSIIYVKMLANIFNKDKAISFLGCMVQFYLFCTCVVTEVFLAVMAYDRYVAICNPL  
 LYTVTMSWKVRVELASCCYFCGTVCSLIHLCLALRIPFYRSNVINHFCDLPVLSLACSDITVN  
 ETLFLVATLINESVTIMILTSYLLILITILKMGSAEGRHKAFSTCASHLTATVFHGTVLSIYCRP  
 SSGNSGDADKAVTVFYTVIPMLNSVIYSLRNKDVKEALRKVMGSKIHS (SEQ ID NO: 9)

40 ATGGGCAAGGAAAACTGCACCACTGTGGCTGAGTTCATTTCTCCTTGGACTATCAGATGTC  
 CTGAGTTGAGAGTCTGCCTCTTCTGCTGTCTCTCTCATCTATGGAGTCACGTTGTAGCC  
 AACCTGGGCAATGATGCACTGATTCAGGTACGCTCTCGGCTCCACACCCCATGTACTTTT  
 TCCTCAGCCACTTGTCTCTGTAGATTCTGCTACTCTCAATAATTGTGGCAAAAAATGTG  
 GCTAATATCTTAAACAGGACAAAGCCATCTCCTTCTAGGGTGCATGGTGCAATTCTACT  
 TGTTTTGCACTTGTGTGGTCACTGAGGTCTTCTGCTGGCCGTGATGGCCTATGACCGCTTT  
 GTGGCCATCTGTAACCCCTTGTCTATACACAGTCACCATGCTTGGAAAGTGTGCTGGAGC  
 45 TGGCTTCTGTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCATTGTGCTTAGCTCT  
 AGGATCCCTCTATAGATCTAATGTGATTAACACACTTTTCTGTGATCTACCTCTGTCTT  
 AAGTCTTGCTTGCTGTATCACTGTGAATGAGACACTGCTGTCTCTGGTGGCCACTTTG  
 AATGAGAGTGTATACCATCATGATCATCTCACTCTCACTCTCACTGCTCACTCACTCACT  
 GAAGATGGGCTCTGACAGGGGACAGGACAAAGCCCTTCCACCTGTGCTTCCACCTCACCA  
 50 GCTATCACTGTCTTCCATGGAAACAGTCTTCCATTATTGTACAGGCCAGTTCAGGCAATA  
 GTGGAGATGCTGACAAAGTGCCACCGTGTCTACACAGTCGTGATTCTATGCTGAACCTC  
 TGTGATCTACAGCCTGAGAAAATAAGATGTGAAGAAAGCTCTCAGAAAAGTGATGGGCTC  
 CAAAAATCACTCTAG (SEQ ID NO: 10)

**AOLFR6 sequences:**

MMASERNQSSSTPIFILLGFSEYPEIQVPLFLVFLVYTVTVVGNLGMIIIRLNSKLHITIMYFFLS  
HLSLTDPCFSTVVPKLLLENLVEYRTISFSGCIMQPCFACIFGVTEIFMLAAMAYDRFVAVCK  
5 PLLYTTTMSQKLCALLVAGSYTWGVCSLILTYFLDLLSCFESTFINNFICDHSVIVSASYSDDPYIS  
QRLCFIAIFNEVSSLIIILTSYMLIFTTIMKMRASGRQKTFSTCASHLTATIFHGHTILFVYVCPNP  
KTSLSLIVTASVFYTVAIPLMLNPLIYSLRNKDINNMFELKLVVTKLIYH (SEQ ID NO: 11)

ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATTCTCTGGGTTTTTCAG  
AATACCAGAAATCCAGGTTCCACTCTTTCTGGTTTCTTGTTCTGCTACACAGTCACTGTA  
10 GTGGGGAACCTTGGGCATGATAATAATCATCAGACTCAATTCAAAACTCCATACAAATCATGT  
ACTTTTTCCTTAGTCACTTGCCITGACAGACTTCTGTTTTCCACTGTAGTACACTAAA  
CTGTTGGAGAACTTGGTTGTGGAATACAGAACCACTCTCTTCTCGGTTGCATCATGCAAT  
TTTGTTTTGCTTGCATTTTGGAGTGACAGAAACTTTCATGTTAGCAGCGATGGCTTATGAC  
CGTTTTGTGGCAGTTTGTAAACCTTGCTGTATACCACATTTATGCTCAGAAAGCTCTGTGC  
15 TCTTCTGGTGGCTGGGCTCTATACATGGGGGATAGTGTGCTCCCTGATACACTACATATTT  
CTTCTTGACTTATCGTTTTGTGAATCTACCTTCATAAAATAATTTATCTGTGACCACTCTGT  
AATTGTTTCTGCTCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTTTATTATTGCCA  
TATTCAATGAGGTGAGCAGCCTAATTATCATTCTGACATCATATATGCITATTTCTCACTACC  
ATTATGAAGATGCGATCTGCAAGTGGGGCGCCAGAAAACTTTCTCCAGCTGTGCCCTCCACC  
20 TGACAGCCATCACTATCTTCCATGGAACATCTGCTTTCTTACTGTGTCTCTAATCTCAAAA  
ACTTCTAGCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGGCGATTCCAATGTGTA  
ACCCATTGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAAATTAGTTGT  
CACCAAAATTGATTTACCACTGA (SEQ ID NO: 12)

**AOLFR7 sequences:**

MSYFYRLKLMKEAVLVKLPFTSLPLLQTLRSRSDMEIKNYSSSTSFGILLGLSSNPOLQKPLF  
AIFLIMYLLAAVGNVLIIPIYSDPRLHTPMYFFLSNLSFMDICTTIVVPKMLVNFSETKVISY  
VGRCLAQMYFFMAFGNTDSYLLASMAIDRLVAINCPHLHYDVMKPRCLLMLLGSCSIIHLHSL  
FRVLLMSRLSFCASHIHKFFCDTQPVCLKLSCDTSQQMVVMTETLAVIVTPFLCIIFSYLRIMV  
30 TVRLRPSAAGKWKAFSTCGSHLTAVALFYGSIIYVYFRPLSMYSVVRDRVATVMYTVVTPMLN  
PFIYSLRNKDMKRGKLKLQDRIYR (SEQ ID NO: 13)

ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAAGCTGCTTGGTCAAACCTGCCCTTTA  
CATCTCTCCCACCTGCTTCTCCAAACCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA  
35 ATACAGCAGCAGCACTCAGGCTTCATCTCTCGGCTCTCTTCCAACCTCAGCTGCAG  
AAACCTCTCTTTGGCATCTTCTCTCATCATGTACCTGCTCGCTGCGGTGGGGAATGTGCTCAT  
CATCCCGGCCATCTACTCTGACCCCAAGGCTCCACAGGCTATGTACTTTTTCTCAGCAAACT  
TGCTTTTCATGGATACTGCTTCAACAACAGTCATAGTGCCATCGACCGGCTGGTGGCAATTTCTA  
40 TCAGAGACAAAGGTTATCTCCTATGTGGGCTGCCTGGCCAGATGTACTCTTTATGGCAT  
TTGGGAACACTGACAGCTACCTGCTGGCTCTATGGCCATCGACCGGCTGGTGGCCATCTG  
CAACCCCTTACACTATGATGTGGTTATGAAACCACGGCATTGCTGCTCATGCTATTGGGTT  
TCTTGCAGCATCTCCCACTACATCTCCCTGTTCCGCTGCTACTTATGCTCTGCTTTGCTTT  
CTGTGCTCTCAGCATCTAATAGCACTTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT  
GCTCTGACACATCTCTCAGCCAGATGGTGGTGTAGTACAGACCTTAGCTGTCAATTGTGAC  
45 CCCCTTCTGCTGTATCATCTTCTCCTACCTGCGAATCATGTGCTGTGCTCAGAACTCCCT  
CTGACGCGGGGAAGTGAAGGCTTCTCTACCTGTGGCTCCCACTCACTGCAGTAGCCCT  
TTTCTATGGGAGTATTTATGTCTATTTAGGCGCCGTGCTCATGTACTCAGTGGTTAGGG  
ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCCTTTCATCTACAG  
50 CCTGAGGAACAAAGATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAAATTACCGGTA  
A (SEQ ID NO: 14)

**AOLFR8 sequences:**

MATSNHSSGAEFILAGLTQRPELQLPLFLFLGIYVVTVVGNLGMIFLIALSSQLYPPVYVYFLSH  
LSFDILCYSSVITPKMLVNFVPEENIISFLEICTQLYFFLIFVIAEGYLLTAMEYDRVYVACRPLLY  
55 NIVMSHRVCSSIMAAVYSSLGFLWATVHTTRMSVLSFCRSMTVSHYFCDLPLLTLCSSSHINEI

LLFIIGGVNTLATTLAVLISYAFIFSSILGIHSTEGQSKAFGTCSSHLLAVGIFFGSITFMFKPPSS  
TTEMEKEKVSSVFYTHIPLMLNPLIYSLRNKDVKNALKKMTIRGRQSS (SEQ ID NO: 15)

5 ATGGCTACTTCAAACCACTTCTCAGGGGCTGAGTTTATCTCTGGCAGGCTTGACACAACGCC  
CAGAAGCTTCAACCTGCCACTCTTCTCTGTTCTCTGGAAATATATGTGGTCACAGTGGTGGG  
GAACCTGGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTTACCCCTCAGGTATATTAT  
TTCTCAGTCATTGTCTTTTCATTGATCTCTGCTACTCTCTGTCACTTACCCTTAAGATGCTG  
7 GTGAACCTTTGTTCCAGAGGAGAACATTATCTCCTTTCTGGAAATGCATTACTCAACTTTATTT  
CTTCTCTATTTTGTAAATTGCAGAAAGGCTACCTTCTGACAGCCATGGAAATATGACCGTTAT  
10 GTTGCTATCTGTGCGCCACTGCTTTACAATATTGTCATGTCCACAGGGTCTGTTCCATAAT  
GATGGCTGTGGTATACTCACTGGGTTTCTGTGGGCCACAGTCCATACACCGCATGCTCA  
GTGTGTGCTACTTGTAGGCTCATACGGTCAGTCATTATTTTGTGATATCTCCCTTATTT  
GACTCTGTCTTGTCTCAGCACCCACATCAATGAGATTCTGCTGTTCAATTATTTGAGGAGTT  
AATACCTTAGCACTACACTGGCGGCTCTTATCTCTTATGCTTTTCTCTAGTATCTCT  
15 TGGTATTCATTCCACTGAGGGGCAATCCAAAGCCTTGGCACTGTAGCTCCCATCTCTGT  
GCTGTGGGCATCTTTTGTGGTCTATAACATTCATGTATTTCAAGCCCTTCCAGCACTAC  
TATGGAAAAAGAGAAGGTGTCTTCTGTGTTCTACATCAAAATAATCCCATGCTGAATCT  
CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCATGAAGAAGATGACTAGGGGA  
AGGCAGTCATCTGA (SEQ ID NO: 16)

20

**AOLFR9 sequences:**

MLARNNSLVTEFILAGLTDPRPEFWQPPFFLFLVIYIVTMVGNLGLITLFLGNLSHLHTPMYYFLFN  
LSFDLCYSSVFTPKMLMNFVSKNIIISNVGCMTRLFFLFFVISECYMLTSMAYDRYVAICNPL  
LYKVTMSHQVCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANIINHLYCDILPLLQLSCTSTYV  
25 NEVVVLVVGNTNITVPSCITILISYVFIVTSLIHKISTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY  
SSGSMEQGKVFSVFYTNVPMNLPLIYSLRNKDVKNALRKALIKIQRNRIF (SEQ ID NO: 17)

30 ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATCTTGTCTGGATTAACAGATCGTC  
CAGAGTTCTGGCAACCCCTCTTTTCTGTCTCTAGTGATCTACATTGTCAACATGGTAGGC  
AACCTTGGCTTGATCACTCTTTCCGGTCTAAATCTCACCTCCACACCAATGACTATTAT  
CCTCTTCAATCTCTCCTTCATTGATCTCTGTACTCTCTGTTTTCACTCCCAAAATGCTAAT  
GAACCTTGTGTCAAAAAAGAATATTATCTCCAATGTTGGGTGCATGACTCGGCTGTTTTTC  
TTTCTCTTTTTCGTCACTCTGGAATGTTACATGTTGACCTCAATGGCATATGATCGCTATGT  
35 GGCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTCTTATGCTCA  
CTTTTGTCTGTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGATGTTTAG  
ACTCACCTCTCGCAGTGCTAATATCATTAAACATACTTGTGTGACATACTCCCCCTCTCC  
AGCTTCTTCCGACAGCACTATGTCAACGAGGTGGTTGTTCTGTGTGGGTACTAA  
TATCACGGTACCCAGTTGTACCATCTCTATTCTTATGTTTTCATTGTCACTAGCAATCTTC  
ATATCAAATCCACTCAAGGAAGATCAAAGCCCTCAGTACTGTAGCTCTCATGTCACTATGC  
40 TCTGTCTCTGTCTTTTGGGTGAGCGGCATTCATGTATATAAATATCTCTTGGATCATGG  
AGCAGGGAAGAAAGTTTCTGTCTTCTACACTAATGTGGTGCCCATGCTCAATCCCTCATC  
TACAGTTTGAGGAACAAGGATGTCAAAGTTGCATGAGGAAAGCTGATTAAATTCAG  
AGGAGAAATATATTCTAA (SEQ ID NO: 18)

45 **AOLFR10 sequences:**

MLARNNSLVTEFILAGLTDPRFQPLFFLFLVIYIVTMVGNLGLIILFGLNLSHLHTPMYYFLFN  
SFIDLCYSSVFTPKMLMNFVSKNIIISNVGCMTRLQFFLFFVISECYMLTSMAYDRYVAICNPL  
KVTMSHQVCSMLTFAAYIMGLAGATAHTGCMRLRLTFCSANIINHLYCDILPLLQLSCTSTYV  
50 EVVVLVVGINIMVPSCTILISYVFIVTSLIHKISTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY  
SGSMEQGKVSSVFYTNVPMNLPLIYSLRNKDVKNALRKALIKIQRNRIF (SEQ ID NO: 19)

ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATCTTGTCTGGATTAACAGATCGTC  
CAGAGTTCTGGCAACCCCTCTTTTCTGTCTCTAGTGATCTACATTGTCAACATGGTAGGC  
AACCTTGGCTTGATCACTCTTTCCGGTCTAAATCTCACCTCCACACCAATGACTATTAT  
55 CCTCTTCAATCTCTCTTCACTGATCTGTACTCTCTGTCTTCACTCCCAAAATGCTAAT  
GAACCTTGTATCAAAAAAGAATATTATCTCTATGTTGGGTGCATGACTCAGCTGTTTTTCT

TTCTCTTTTTCGTACATCTCTGAATGCTACATATTGACCTCAATGGCATATGATCGCTATGTG  
GCCATCTGTAATCCATTGCTGTATGAAGGTCAACCATGTCCCATCAGGCTGTGTTCTATGCTCAC  
TTTTGCTGCTTACATAAATGGGATTGGCTGGAGGCCACGCCACACCGGGTGCAATGCTTAGA  
CTCACCTTCTGCAGTGCTAATATCATCAACCATTACTTGTGTGACATACTCCCCCTCTCCA  
5 GCTTTCTGCGACCGACCACTATGTCAACGAGGTGGTGTGTTCTCATTGTTGTGGGATTAAT  
ATCATGGTACCCAGTTGTACCATCTCATTTCTTATGTTTTCATGTGCACTAGCATCTTCTCA  
TATCAAATCCCACTCAAGGAAGATCAAAGGCCTTCAGTACTTGTAGCTCTCTCATGTCAATGCT  
CTGCTCTGCTTTTGGGTACAGCGGCATTCATGTATATAAATATCTCTTGGAATCTATGGA  
10 GCAGGGAAAGGTTCTCTGTTTCTACATAATGTGGTGCCCATGCTCAATCCCTCTCATCT  
ACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAATAATTCAGA  
GAAGAAATATATTCTAA (SEQ ID NO: 20)

# **AOLFR11 sequences:**

MTLRNSSSVTEFILVGLSEQPELQLPLFLLFLGIYVFTVVGNLGLITLIGINPSLHTPMYFFLNL  
15 FIDLCSYCVFTPKMLNDFVSESHSYVGCMTQLFFCFVNSECVLVSMAYDRYVAICNPLLY  
MVTMSPRVCFLLMFGSVVVGAGAMAHTGSMRLRTFCDNSVIDHYLADVLQLQLSCSTSTHV  
SELVFFIVVGTMLSSISIVISYALILSNILCPSAEGRSKAFSTVGSIHJAVLFFGSGTCTYLTTS  
FPGSMNHRGFASVFTYNNVPMNLNPSIYSLRNKDDKLALGKTLKRVLF (SEQ ID NO: 21)

20 ATGACTCTGAGAAACAGCTCCTCAGTGACTGAGITTTATCCTTGTGGGATTATCAGAACAGC  
CAGAGCTCCAGCTCCCTCTTTCTCTTCTATTCTTAGGGATCTATGTGTTCACTGTGTTGGGCG  
AACTTGGGCTTGATCACTTAATTTGGGATAAACTCAGCTTACACACCCCATGTACTGTTTCT  
CCTCTTCAACTTGTCTTTATAGATCTCTGTTATTCCTGIGTGTTTACCCCAAAATGCTGA  
25 ATGACTTGTGTTCAGAAAGTATCATCTCTTATGTGGGATGATGACTCAGCTATTTTTCTTC  
TGTTTCTTTGTCAATTCTGAGTGCTATGTGTGGTATCAATGGCCATGATGCTGATGTGGC  
CATCTGCAACCCCTGCTCTACATGGTCAACATGTCCCAAGGCTTCTGCTTCTGCTGATGT  
TTGGTTCTATGTGTAGGTTTGTCTGGGCGCATGGCCACACTGGAAGCATGCTGCGACT  
GACCTCTGTGATTCACACGTCTTGACCATTAATCTGTGTGACGTTCTCCCCCTTCTGCAGC  
30 TCTCTGCAACGACCACTGTCAGTGAGCTGGTATTTTTCATTGTTGTGTGGAGTAACTCAC  
ATGCTATCCAGCAATAAGCATCGTCATCTCTTACGCTTTGATACTCTCAACATCTCTGAT  
TCCTTCTGCAAGAGGCGAGATCCAAAGCCTTTAGCACATGGGGCTCCCAACATAATGTGCTGT  
GCTCTGTTTTTGGGTCAAGGACATTCACCTACTTAACAACATCTTTCTGGCTCATGTAA  
CCATGGGAGATTGCTCATGCTTTTACACCAATGTGGTTCCCATGCTTAACCCCTTCGATCT  
35 ACAGTTTGAGGAATAAGGATGATAAATTCGCCCTGGGCAAAACCCCTGAAGAGAGTGCTCT  
TCTAA (SEQ ID NO: 22)

# **AOLFR12 sequences:**

MERNHNPDCNVNLFNFFADKKNKRRNFGQIVSDVGRICYSVLSLGEPTTMGRNNLTPSEFIL  
LGLSSRPEDQKPLFAVFLPYLITVIGNLLIILAIRSDTRLQTPMYFFLSLSFVDICYVTVIIPKMLV  
40 NFLSETKTISYGECLTQMYFFLAFGNTDSYLLAAMADRYVAICNPFHYITIMSHRCCVLLLVLS  
FCPIPHFSLHLLHLLTNQLIFCASNVIIHFFCDDQPVKLSCSSHVFVKEITVMTBGLAVIMTPFSCIII  
SYLRILITVTKIPSAAGKRAFTSCGSHLTVVTLFYGSISYVFPQLPSNYTVKDQIATIIYTVLTP  
MLNPFYISLRNKDMKQGLAKLMHRMKCQ (SEQ ID NO: 23)

45 ATGGAAGAAACCACAAATCCAGATAATTGTAATGTTTTAAATTTTTTCTTGTGATGAAGA  
AGAATAAAAGGAGAAATTTGGACAGATGTATCAGATGTTGGAAGAATCTGTTACAGTG  
TAGTTTATCTTTAGGTGAACCCCACTATGGGAAGAAATAACCTTAACAAGACCCCTCTGA  
ATTACCTCTCTTGGACTCTCCTCTCGACCTGAGGATCAGAAGCCGCTCTTTGCTGTGTTCC  
TCCCACTCTACCTTATCAGAGTATAGGAAACCTGCTTATCATCTCTGGCCATCCGCTCAGA  
50 CACTGCTCTCAGACGCCCATGTACTCTTTCTAAGCATCTCTTTTGTGACATTGTGT  
ATGTGACAGTCATTACCTCAAGATGCTGGTGAACCTCTTATCAGAGACAAAGACCATCTC  
TTACGGTGAGTGTCTGACCCAGATGTACTTTTTCTTAGCCCTTGGAACACAGACAGATTAC  
CTGCTAGACGCTATGGCCATTGACCGCTATGTGGCCATATGTAATCCCTTCCACTACATCA  
CCATTATGAGTGCACAGATGCTGTGCTGCTCTGCTGTTCTCTCTTGCATTCACATTTT  
55 CACTCCCTTGCACATTTCTCTGACTAATCAGCTCATCTCTGTGCTCTCAATGTATCCA  
TCACTTTTCTGCGATGATCAACAGTGCTAAATTTGCTGTTCTCTCCCATTTTGTCAAAG



AAATCACAGTAATGACAGAAGGCTTGGCTGTCTATAATGACCCCGTTTTTCATGCATCATCAT  
CTCTTATTTAAGAACTCTCATCACTGTTCTGAAGATTCTTCAGCTGCTGGAAAGCGTAAAG  
GCATTTTCTACCTGTGGCTCTCATCTCACAGTGGTGACCCCTGTTTATGGAAGCAATAGCTA  
TGTCTATTTTTCAGCCCTGTCCAACATACTGCAAGGATCAAATAGCAACAATATCTAC  
5 ACCGTATGACTCTATGCTAAATCCATTTATCTATAGTCTGAGGAGCAAAAGACATGAAGC  
AGGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

#### AOLFR13 sequences:

MDQKNGSSFTGFILLGFSDRPQLELVLFVLLIFYFTLLGNKTIIVLSHLDPHLHNPYFFFSNL  
10 SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLGSTCVLLGVMAFDRYAAVCRPL  
HYTVVMHPCLYVLMASTSWVIGFANSLQLVLILLTLCGRNKLEHFLCEVPPLKLKACVDTT  
MNESELFVSVIILLVPVALIIFSYSQIVRAVVRKISATGQRKVFGTCGSHLTVVSFLFYGTAIYAY  
LQPGNNYSQDQGXISLFYTIITPMINPLIYTLRNKDVKGALKKVLWKNYDSR (SEQ ID NO:  
25)

15 ATGGATCAGAAAAATGGAAGTTCTTCACTGGATTTATCTCACTGGGTTTCTCTGACAGGC  
CTCAGCTGGAGCTAGTCCTCTTTGTGGTTTCTTTGATCTCTATATCTTCACTTTGCTGGGG  
AACAAAACCATCATTTGTAATTATCTCACTGGACCCACATCTTCAACAATCCTATGTAATTTTT  
CTTCTCCAACCTAAGCTTTTGGATCTGTGTACACACCCGGCATGTTCACAGCTCCTGG  
20 TTAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGATTCAGTGTACAT  
CTCTCTAGGCTTGGGATCTACAGAATGCGTTCTCTTAGGAGTGATGGCATTTGACCGCTAT  
GCAGCTGTTTTCAGGCCCTCCACTACACAGTAGTCATGCACCTTGTCTGTATGTGCTGA  
TGGCTTCTACTTCTATGGGTCTTGGTTTGGCAACTCCCTATTGCAGACGGTGCTCATCTTG  
CTTTAAACACTTTTGTGGAAGAAATAAATTAGAACACTTTCTTTGTGAGGTTCTCCATTTGCT  
25 CAAGCTTGCCTGTGTGACACTACTATGAATGAATCTGAACCTCTTTGTGACGTGCATTA  
TCTTCTTGTACTGTTCATTAATCATATTCTCTATAGTCAGATTGTCAGGGCAGTCTGTG  
AGGATAAAGTCAGCAACAGGGCAGAGAAAAGTGTGGGACATGTGGCTCCCACTCAGCA  
GTGGTTTCCCTGTTCTACGGCACAGCTATCTATGCTACCTCCAGCCGGCAACAACACTACTC  
TCAGGATCAGGGCAAGKTCATCTCTCTCTACACCATCATTACACCATGATCAACCCCT  
30 CTCATATATACACTGAGGAACAAGGATGTGAAAGGAGCATTAAGAAGTGCTCTGGAAG  
AACTACGACTCCAGATGA (SEQ ID NO: 26)

#### AOLFR14 sequences:

MALPLLSSPSFCASSQSLSSRMNSENLTAAAVAPAEFVLLGITNRWDLRLVALFTCLPVYVLSL  
35 LGNMGALLLRMDARLHTPMYFFLANLSLLDACYSSAIGPKMLVDLLPRATIPYTCALQMF  
VFAGLADTECCLLAAMAYDRYVAIRNPLYYTAMSQRCLCALLGASGLGGAVSFAVHTTLTF  
RLSFCRSRKINSFFCDIPPLLAISCDTSLNELLFAICGFIQTAVLAHTVSYGFIAGA VIHMRSEV  
GSRRAASTGGSHLTAVAMMYGTLIFMYLRPSSYALDDKMASVFYTLVIPS LNPLIYSLRNKE  
VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

40 ATGGCCTTGCCATTGCTCTTATCTCCCTCCTGCTTTGCCCTTCTCTCAGTCTCTGTCCAGTAG  
GATGAACCTCAGAGAACCTCACCCGGGCGCGGTTGCCCTGCTGAATTGCTCTCTCGGGC  
ATCACAATCGCTGGGACCTGCGTGTGGCCCTCTCTGACCTGCTCCTGCTGTCTACCTGTG  
TGAGCGCTGCTGGGAACAATGGGCATGGCGCTGCTGATCCGATGGATGCCCGGCTCCACA  
45 CAOCCTATGACTTCTCTGGCAACCTCTCCCTGCTGGATGCCTGCTATCTCCGCACTC  
GGCCCCAAGATGCTAGTGGACCTGCTGCTGCCCGAGCCACCATCCCTTACACAGCCTGTG  
CCCTCCAGATGTTGTCTTTGACAGTCTGGCTGATGACTGAGTGTGCTTGTGGCAGCCAT  
GGCCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATACAACAGCTATGTCGAG  
CGTCTATGCTCGCCTTGTCTGGGAGCATCAGGCCTGGGTGGGGCAGTGAGTGCCTTTGTTC  
50 ACACAACCCCTACCTTCCGCTGAGCTTCTGCGCTCCCGGAAGATCAATGAGTCTTCTG  
CGATATCCCTCACTGCTGGCCATCTCGTGCAGTGACACAGTCTCAATGAACATCTCTCTCT  
TCGCCATCTGTGGCTTCTACAGACAGCCACGGTGTTAGCTATCAGGTGCTTATGGCTT  
CATCGCTGGGGCTGTGATCCACATGCGCTCGGTGAGGGCAGTGGCGAGCAGCCTCCAC  
CGGTGGTTCCCACTCAGACCGTGGCCATGATGTACGGGACACTATTTTCATGTACCTG  
55 CGCCCACTCCAGATGCCCTGGACACTGACAAGATGGCCTCTGTGTTCTATACCCCTGG

TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT  
CAGGCAGACCTGGAGCCGATTCCACTGTCCAGGGCAGGGGTCCCAGTGA (SEQ ID NO: 28)

**AOLFR15 sequences:**

5 MRENNSSTLEFILLGVTGQQEQEDFFYLFLFYIPITLIGNLLIVLAICSDVRLHNPMYFLLANLS  
LVDIFFSSVITPKMLANHLTGSKSISFGGCLTQMYFMIALGNTDSYLAAMAYDRAVAISHPLH  
YTTIMSPRSCIWLAGSWVIGNANALPHLLTASLSFCGNQEVANFYCDITPLKLKSCSDIHFHV  
KMMYLGVGFSPLLCIIVSYIRVFSTVFQVPSTKGVLFKAFSTCGSHLTVVSLYYGTVMGTYFR  
PLTNYSLKDAVITVMYTAVT PMLNPFYSLRNRDMKAALRKLFNKRIS (SEQ ID NO: 29)

10

ATGAGGGAAAAATAACCACTCTCTACACTGGAATTCATCTCTGGGAGTTACTGGTCAGC  
AGGAACAGGAAGATTTCTTCTACATCTCTTCTGTTCAATTACCCCATCACATTGATTGGA  
AACCTGCTCATTTGCTAGCCATTTGCTCTGATGTCGCCCTCACAAACCCCATGTATTTCT  
15 CCTTGCCAACTCTCTCTGGTGGACATCTTCTTCATCGGTAACCATCCCTAAGATGCTGG  
CAACACCATCTCTTGGGCAGCAAAATCCATCTCTTTGGGGGATGCCTAACCGCATGTATTT  
CATGATAGCCTTGGGTAAACACAGACAGCTATAATTGGCTGCAATGGCATATGATCGAGCT  
GTGGCCATGACGCCACCCACTTCACTACACAACAATATGAGTCCACGGCTTGTATCTGGC  
TTATTGCTGGGTCTTGGGTGATTTGGAATGCCAATGCCCTCCCCACACTCTGCTCACAGC  
TAGTCTGTCTCTTGTGGCAACCCAGGAAGTGGCCAACTTCACTGTGACATTACCCCTTG  
20 CTGAAGTTATCCTGTTCTGACATCCCACTTCACTGTGAAGATGATGTACCTAGGGGTGGCA  
TTTCTCTGTGCCATTACTATGCATCATTGTCTCTATATTGAGTCTTCTCCACAGTCTTCC  
AGGTTCTCTCCACCAAGGGCGTGCTCAAGGCCCTTCCACCTGTGGTTCACCACTACGGT  
TGCTCTTTGTTATTAGTGATACAGTCAATGGGCAGTATTTCCGCCCTTTGACCAATTATAGCC  
TAAAGAGCGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTTAAATCCTTTCAT  
25 CTACAGCTGAGAAATCGGGACATGAAGGCTGCCCTCGGGAACCTTCAACAAGAGAAT  
CTCCTCGTAA (SEQ ID NO: 30)

**AOLFR16 sequences:**

30 MRRNCTLVTEFILLGLTSRRELQILLFTFLAIYMTVAVAGNLMIVLIQANAWLHMPMYFELSH  
LSFVDLCFSSNVTPKMLEIFLSEKKSISYPACLVCYQLFIALVHVEIYILAVMAFDTRYMAIGNPLL  
YGSRMKSVCFLITVPYVYGALTGLMETWYTNLAFCEGPNINHFCADPPLIKLACSDTYN  
KELSMFIVAGWNLSFLFIICISYLYIFPAILKIRSTEGRQKAFSTCGSHLTAVTIFYATLFFMYLR  
PPSKESVEQGMVAVFYTTVIPMLNLIYSLRKNVKEALIKELSMKIYFS (SEQ ID NO: 31)

35 ATGAGAAGAACTGCACGTTGGTGACTGAGTTCATTCTCTGGGACTGACCAAGTCGCCGG  
GAATTACAAATTCCTCTTCAAGCTGTTCTCGGCCATTTACATGGTCAAGGTGGCAGGGA  
ACCTTGGCATGATTTGTCTCATCCAGGCCAACGCCTGGCTCCACATGCCCATGTACTTTTCT  
CTAGGCCACTATCCTTCGTGGATCTGTGCTCTCTTCCAATGTGACTCCAAGATGCTGG  
AGATTTTCTCTTCAGAGAAGAAAAGCATTTTCTATCTGCCTGTCTTGTGCAAGTGTACCTT  
40 TTTATCGCCTTGTTCATGTTGAGATCTACATCTCGGCTGTGATGGCCCTTGACCGGATACAT  
GGCCATCTGCAACCTCTGCTTTATGGCAGCAGAAATGTCCAAGAGTGTGTGCTCTTCTC  
ATCACGGTGCCTTATGTGATGGAGCGCTCACTGGCCTGATGGAGACCATGTGGACCTACA  
ACCTAGCCTCTGTGGGCCCAATGAAATTAATCACTTCTACTGTGCGGACCCACCACTGAT  
TAAGCTGGCTGTGTTCTGACACCTACAACAAGGAGTTGTCAATGTTATTGTGGCTGGCTGG  
45 AACCTTCTTTTCTCTTTCATCATATGATATTCTCACTTTACATTTTCTCTCTCTATTTTA  
AAGATTGCTCTACAGAGGGCAGGCAAAAGCTTTTCTACCTGTGGCTCCCATCTGACAG  
CTGTCACTATATTCTATGCAACCTTTCTTCTCATGTATCTCAGACCCCTCAAGGAATCT  
GTTGAACAGGCTAAAAATGGTAGCTGTATTTATACCAAGTAATTCCTCTGTCAACCTTA  
TAATTTATAGCCTTAGAAAATAAAATGTAAAGAAGCATTAATCAAGAGCTGTCAATGA  
50 AGATATACTTTTCTTAA (SEQ ID NO: 32)

**AOLFR17 sequences:**

MLNFTDVTEFILLGLTSRREWQVLFHIFLVVYIITMVGNGIMMVLIKVSPQLNNPMYFELSHLS  
FVDVWFSSNVTPKMLENLFSDDKTTITYAGCLVQCFFIALVHVEIFILAAMAFDRYMAIGNPLL  
55 YGSKMSRVV CIRLITFPYVYGFLLSLAATLWTYGLYFCGKIEINHFCADPPLIKMACAGTFVKE

YTMIIILAGINFYTSYLVIIISYLFILIAILRMRSAEGRQKAFSTCGSHLTAVIIFYGTLIFMYLRRPTE  
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

5 ATGCTCAATTCACCGATGTGACAGAGTTCATTCTTTGGGGCTAACAGGCCGTCGAGAAT  
GGCAAGTCTCTCTTCATCATCTTTCTGTGGTCTACATCATCCACCATGGTGGGCAATATC  
GGCATGATGGTGTTAATCAAGGTCAGTCCCTCAGCTTAAACAACCCCATGTACTTTTCTCTCA  
GTCACCTTGTCATTGTTGATGTGTGGTCTTCTTCCAATGTCACCCCTAAATAGTTGGAAAAC  
CTGTTTTCAGATAAAAAACAATTACTATGCTGGTGTGTTAGTAGCAGTGTCTTCTTTCAT  
10 TGCTCTTGCCATGTGGAAAATTTTATTCTTGCTGCGATGGCCTTTGATAGATACATGGCAA  
TTGGGAATCCTCTGCTTTATGGCAGTAAAAATGTCAAGGGTTGCTGTATTCCAGTGATTAC  
TTTCCCTATCAATTAATGTTTCTGACGAGTCTGGCAGCAACATTATGGACTACGGCTGTG  
ACTCTGTGGAAAATTTAGATCAACCACTTCTACTGTGCAGATCCACCTCTCATCAAAAT  
GGCCTGTGCCGGGACCTTTGTAAAGAATATACAATGATCATACTTGCCGGCATTAACCTC  
ACATATTCCTGACTGTAATTAATCATCTCTTACTTATTCATCTCTCAATTCGCCATTGCGAAAT  
15 CGCCTCAGCAGAAAGGCAAGGCAAGGCCCTTCCACATGTGGGTGCCATCTGCAGAGCTGT  
CATTATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCCACAGAGGAGTCTGTG  
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGTATCCCCATGTGTAATCCCATGA  
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTATCAGCAGATCAT  
GTTAA (SEQ ID NO: 34)

20

**AOLFR18 sequences:**

MSNTNGSAITEFILLGLTDCPELQSLFLVFLVYVLTLLGNLGMIMLMRLDSRLHTPMYFFLT  
NLAFLVDLCYTSNATPQMSTNIVSEKTIISFAGCTQCYIFIALLLTEFYMLAAMAYDRYVAIYDP  
25 LRYSVKTSRRVVICLATFPYVYGFSDGLFQAILFRLTFCRSNVINHFYCADPPLIKLSCSDTYVK  
EHAMFISAGFNLSLLTIVLVSYAFILAAILRIKSAEGRHKAFTCCGSHMMAVLTFLVGTFCMYK  
RPPTDKTVEESKILAVFYTFVSPVLNPLIYSLRNKDVQKALKNVLR (SEQ ID NO: 35)

30 ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGCC  
CGGAACATCCAGTCTCTGCTTTTGTGCTGTTTCTGGTGTGTTACCTCGTCACCCGTCTAGGC  
AACCTGGGCATGATAATGTTAATGAGACTGCTCGCTCAGCCCTACAGCCCATGTACTTCT  
TCTCTCAACTAGCTTTGTGGATTGTGCTATACATCAATGCAACCCCGCAGATGTC  
GACTAATATCGTATCTGAGAAGACCATTTCTCTTGCTGGTGTGCTTACACAGTGCTACATTT  
TCATTGGCCCTTCTACTCACTGAGTTTACATGCTGGCAGCAATGGCCTATGACCGTATGT  
35 GGCATATATGACCTCTCGCGCTACAGTGTGAAAACGTCAGGAGAGTTGTCATCTGCTTG  
GCCACATTTCCTATGTCTATGGCTCTCAGATGGACTCTCCAGGCCATCCTGACCTTCG  
CCTGACCTTCTGTAGATCCAATGTCTCAACCACTTCTACTGTGCTGACCCGCCGCTCATTA  
AGCTTCTTGTTCTGATACCTATGTCAAAGAGCATGCCATGTTCAATCTGCTGGCTTCAAC  
CTCTCAGCTCCCTCACCATCTGCTTGGTGTCTATGCCCTTCATCTTCTGCTGCCATCTCCG  
GATCAAAATCAGCAGGGGAAGGCACAAGGCATTTCCACCTGTGGTTCCTCATATGATGGC  
40 GTGCACCTGTGTTATGGGACTCTCTTTTGATGTATATAAGACCAACCAACAGATAAGACT  
GTGAGGAATCTAAAAATAATAGCTGTCTTTTACACCTTTGTGAGTCCGCTACTATGATCCAT  
TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCCTGAAGAATGTCTGATAGATGA  
(SEQ ID NO: 36)

45 **AOLFR19 sequences:**

METKNYSSTSGFILLGLSSNPKLQKPLFAIFLIMYLLTAVGNVLILAIYSDPRLHTPMYFFLSNL  
SFMDCFTTIVVPKMLVNFLETKIISYVGCLIQMYFFMAFGNTDSYLLASMAIDRLVAICNPLH  
YDVVMKPPWHCLMLLGGCSISHLHSLFRVLLMSRLSFCASHIHKHFDQTPQLIKLSCSDSSQ  
50 MVMVMTETLAVIVTPFLCTIIFSYLQHVTVLRIPSAAGKWKAFSTCGSHLTVVVLYFGSVVYVYFR  
PLSMYSVMKGRVATVMYTVVTPMLNPFIIYSLRNKDMKRLKLLKLRHRIYS (SEQ ID NO: 37)

ATGGAGACAAAAGATTATAGCAGCAGCACTCAGGCTTCATCTCTCTGGGCTCTCTTCCA  
ACCTAAGCTCGAGAAACCTCTCTTGCCATCTTCTCATCATGTACCTACTGACCTGCGGTG  
GGGAATGTGCTCATCATCTGGCCATCTACTGACCCCAAGGCTCCACACCCCTATGACT  
55 TTTTCTCAGCAACTTGCTTTTATCATGGATATCTGCTTCAACACAGTCAATAGTGCCTAAGATG  
CTGGTGAATTTTCTATCAGAGACAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT

ACTTCTTACATGGCCATTGTGGGAACACTGACAGCTACCTGCTGGCCCTCTATGGCCATCGACCG  
GCTGTTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCAITGGCTA  
CTCATGCTATTGGGTTCCTGACGATCTCCACCTACATTCCCTGTTCCGGGTGCTACTTAT  
GTCTCGCTGTCTTCTGTGCTCTCACATCAITTAAGCACTTTTCTGTGACACCCAGCTG  
5 TGCATAAGCTCTCCTGCTCTGACACATCTCCAGCCAGATGGTGGTGATGACTGAGACCTT  
AGCTGTCAITTTGACACCCCTTCTGTGTACCATCTTCTCCTACCTGCAAAATCATGCTCACTG  
TGCTCAGAATCCCTCTGACGCCGGAAGTGAAGGCTTCTCTACCTGTGGCTGCCACCT  
CACTGTAGTGGTCTGTTCTATGGGAGTGATCATCTATGTCTATTTAAGGCCCTGTGCTCATGT  
10 ACTCAGTGATGAAGGGCCGGTAGCCACAGTTATGTACACAGTAGTGACACCATGCTGA  
ACCCCTTCACTACAGCCTGAGGAACAAAGATATGAAAAAGGGTTGAAGAAATTAAGAC  
ACAGAAATTTACTCATAG (SEQ ID NO: 38)

#### AOLFR20 sequences:

MVEENHTMKNEFILTGTFDHPCLKTLLFVVFIAIYLITVVGNISLVALIFTHCRLHTPMYIFLGN  
LALVDSCCCATAITPKMLNFFSEBGRISLYEBCAQFYFLCTVETADCFLLAAVAYDRYVAICNP  
15 LQYHIMMSKKLQIOMTTGAFIAGNLHSMIHVGLVFLRFVCGLNHNHNYCDTLPLYRLSCVDPP  
INELVLFIHSGSVQCTTFSVLISLYILLTIFRMKSEGRAKAFSTCAHSFSSVSLFVYSGIFLYIRP  
NLLEEGNDIPAAILFTIVVPLNPFHYSRLNKEVISVLRKILLIKISQGSVKN (SEQ ID NO: 39)

20 ATGGTTGAAGAAAATCATACCATGAAAAATGAGTTTATCTCAGAGGATTACAGATCACC  
CTGAGCTGAAGACTCTGCTGTTGTGGTGTCTTGTGCCATCTATCTGATCACCCTGTGGGG  
GAATATATAGTTTGGTGGCACTGATATTTACACACTGCTCGGTTACACACCAATGTACATC  
TTTCTGGGAAATCTGGCTCTTGTGGATTCTTGCTGTGCTGTGCTATTAACCCCAAAATGTT  
AGAGAAATCTTTTCTGAGGGGCAAAAGGATTTCCTCTATGAATGTGCAGTACAGTTTAT  
25 TTTCTTTGCACTGTGGAAACTGCAGACTGCTTTCTTGGCAGCAGTGGCCTATGACCGCT  
ATGTGGCCACTCTGCAACCCACTGCAGTACCACATCATGATGTCCAAGAAATCTGCATTCA  
GATGACCAAGGCGCTTTCATAGCTGGAATCTGCATTCATGATTATCATGTAGGCGTGTGA  
TTTAGGTTAGTTTCTGTGGATTGAATCAATCAACCACTTTTACTGTGATACITCTCCCTT  
GTATAGACTCTCCTGTGTGACCCCTTTCATCAATGAACCTGGTTCTATTATCATCTCTCAGGTT  
30 CAGTCAAGTCTTACCATAGGTAGTGTCTAATATCTTATCTCTATCTCTTACTIAT  
TTCAGAAATGAAATCCAAGGAGGGAAGGGCCAAAGGCTTTTCTACTTGTGATCCCACTTTT  
CATCAGTTTCATATTCTATGGATCTATTTTTTCTTATACATAGACCAAAATTTGCTTGAA  
GAAGGAGGATATGATATACAGCTGCTATTATTTTCAATAGTAGTTCCTCTACTAAATC  
35 CTTTCAATTATAGTCTGAGAAACAAAGGAAGTAATAGTGTTCTTAAGAAAAATTCGTGTAA  
AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

#### AOLFR21 sequences:

MEPRKNVDFVLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVVTVTSETLGSPMSFFLAGL  
TFIDIIYSSSIPRLISDLFGNNSISFQSFMALFIEHLFGGSEVFLLLVMAYDRYVAICKPLHYLV  
10 IMRQVGVCLLLVSVWGGLQSVFQLSIYGLPFCGPNVIDHFFCDMYPLCLKLACTDTHVIGLL  
VVANGGLSCTIAFLLLISYGVILHSLKKLSQKGRQKAHSTCSSHTTVVVFVFCIFMCRPAR  
TFSIDKSVSVFYTVITPMLNPLIYTLRNSMTSAMKKL (SEQ ID NO: 41)

45 ATGGAGCAAGGAAAAATGTGACTGACTTTGTCTCTTGGGCTTCACACAGAATCCAAAG  
GAGCAGAAAGTACTTTTGTATGTCTTGCTTCTACATTTGACCATGGTGGGCAACT  
GACTATTGTAGTACCGTAACCTGTCAGTGAGACCTGGGCTCACCATGTCTCTTCTTCTT  
GCTGGCTTAACATTTATAGATATCATTTATCTTCATCCATTTCCCCAGATGATTTCAGA  
CTTGTTCTTTGGGAATAATTCATATCCTTCAACTCTTCATGGCCAGCTCTTTATCGAGC  
ACCTTTTGGTGGGTGAGAGGTCTTCTCCTGTGTGGTGATGGCTATGACCCGCTATGTGGC  
50 CATCTGAAGCCCTTGCAATATTGGTTATCATGAGACAATGGGTGTGGTTTGTGCTGCTG  
GTAGTGCTCTGGGTGTGAGGATTCTGCAATCAGTATTTCAACTAGCATATTTATGGGC  
TCCATCTCTGTGGCCCAATGTCAATTGATCATTTTCTGTGACATGTATCCCTATTGAAA  
CTGGCCTGCACTGACACCCATGTTATTGGCCTCTTAGTGGTGGCAATGGAGGACTGTCTT  
GCATCTTGTGGTTCTGTCTCTTACTCATCTCTTATGGTGTCACTCTGCACTCTCTAAGAAA  
55 CTTAGTCAGAAAGGAGGCAAAAAAGCCCACTCAACCTCAGTTCACCATCACTGTGGTGT  
TCTTCTCTTGTCTCTTGTATTTTATGTGTGCTAGACCTGCTAGGACCTTCTCCATTGAC

AAATCAGTGAGTGTGTTTATACAGTCATAACCCCAATGCTGAACCCCTTAATCTACACTC  
TGAGAAATTCTGAGATGACAAGTGCTATGAAGAAGCTTAG (SEQ ID NO: 42)

**AOLFR22 sequences:**

5 MRXXNXTEFVLKFSQDPGVXKALFVMFLITYXXTVVGNLLIVVDIIASPLXGSPMYFFLAC  
LSPIDAAYSTISPLKFLVGLCDKKTISFQGCMMQGLFIDHFFGGAIEVFLLVVMACDRYVAICKPL  
HYLTIMNRQVCVFLLLVXXMIGGFVHSAFQIVVYSLPFCGPXVIVHFSCDMHPLLELACTDTYFI  
GLTVVVVNSGAIMVFIFNLLISYGVILSSLKTYSQEKRKALSTCSSSGTIVVVLFFVPCIFYVRP  
10 VSNFPTDKFMTVFYTIITHMLSPLIYTLRNSMRNAIEKLLGKKLTIHFHGGVSVLM (SEQ ID NO:  
43)

ATGAGACANNNNNAACAATATNACAGAATTGTCTCTCTGGGCTTTTCTCAGGATCCTGGTG  
TGNNAAGAGCAATTATTTGTCATGTTTTTACTCACATACNNNNNNACAGTGGTGGGGAACCT  
15 GCTCATTGTNGTGGATATTATGCCAGCCCTTNNTTGGGTTCGCCAATGTATTTCTCCTTG  
CCTGCCTGTCAITTTATAGATGCTGCATATTCACCTACCAATTTCTCCAAGTTAATTGTAGGC  
TTATTCTGTGATAAAAAGACTATTTCTTCCAAGGTGCATGGGCGAGCTATTTATAGACC  
ATTTCTTTGGTGGGGCTGAGGTTCTCCTTCTGGTGGTGATGGCCTGTGATCGCTATGTGGC  
CATCTGAAGCCACTGCTACTATTTGACCATCATGAATCGACAGGTTTGCCTTCTTCTGTGG  
20 TNNNNCCATGATTGGAGGTTTTGTACATCTGCGCTTTCAAATTTGTGTGTACAGTCCCTCT  
TCTGTGGTCCCNATGTCAATTGTTCAATTTCAAGTTGTGACATGCACCAATCTGGAACCTGGC  
ATGCACGTACACCTACTTTATAGGCTCCTAGTTGTGTGTCATAGTGGAGCAATCTGTATG  
GTCATTTTCAACCTTCTGTTAATCTCCTATGGAGTCACTCAAGCTCCCTTAAACCTACAG  
TCAGGAAGAGGGGTAAAAGCCTTGTCTACCTCGAGCTCCGGCAGTACCCTTGTGTCTCTC  
25 TTTTTGTACCTGTATTTTCATATATGTTAGACCTGTTTCAAACCTTCTCTACTGATAAGT  
CATGACTGTGTTTATACCAATTATCACACACATGCTGAGTCCCTTAAATATACGTGTTGAGA  
AATTCAGAGATGAGAAATGCTATAGAAAACTCTTGGGTAAAAAGTTAACTATATTATTA  
TAGGAGGAGTGTCCGTCCTCATGTAG (SEQ ID NO: 44)

**AOLFR23 sequences:**

30 MAKNNLTRVTEFLMGFMDHPKLEIPLFLVFLSFYLVTLGNVGMIMLIQVDVKLYTPMYFFLS  
HLSLIDACYTSVITPQLAATLATGKTVISYGHCAAQFFLFTICAGTECFLLAVMAYDRYAAIRNP  
LLYTVAMNPRLCWSLVVYAYVCGVSGAILRTTCTFLSPCKDNQINFFCDLPLLLKLACSDTA  
NIEIUIFFGNFVILANASVILISYLLIJKTILKVKSSGGRKATFSTCASHITAVLFFGALIFMYLQS  
35 GSGKSLIEDKVVSVFYTVVPMNLPLIYSLRNKDVKDAFRKVARRLQVLSLM (SEQ ID NO: 45)

ATGGCCAAGAATAATCTCACCAGAGTAACCGAATTCATTCTCATGGGCTTTATGGACCACC  
CCAAATTTGGAGATTCCTCCTCTTCTGGTGTCTCTGAGTTCCTACCTAGTCACCCCTTCTGGG  
AATGTGGGGATGATTATGTTAACTCAAGTAGATGTCAAACCTCACCACCCAATGTACTTCT  
40 TCTGAGCCACCTCTCCTGCTGGATGCCCTGTACACCTCAGTCAATCACCCTCAGATCCTTA  
GCCACATTTGGCCACAGCAAAAACGGTCACTCCTACGGCCACTGTGCTGCCAGTCTCTTT  
TATTACCATCTGTGTCAGGCACAGAGTGCTTTCTGCTGGCAGTGATGGCCTATGATCGCTA  
TGCTGCCATTCGCAACCCACTGCTCTATACCGTGGCCATGAATCCGAGGCTCTGCTGGAGC  
CTGGTGCTAGGAGCTATGCTGTGGGGGTGTGAGGAGCCATCCTGCGTACCACCTATGCACT  
45 TCACCCTCTCCTCTGTGAAGACAATCAAATAAACTTCTCTCTGTGACCTCCCAACCCCTG  
CTGAAGCTTGGCTGCACTGACACAGCAAAACATCGAGATTGTCACTATCTTTGGCAATT  
TTGTGATTTGGCCAATGCCTCCGTCATCTGATTTCCATATCTGCTCATCATCAAGACCAIT  
TTGAAAGGTGAAGTCTCAGGTGGCAGGGGCCAAGACTTCTCCACATGTGCCTCTCACATCA  
CTGCTGTGGCCCTTTCTTTGGAGCCCTTATCTTCATGTATCTGCAAGAGTGCTCAGGCAAA  
50 TCTCTGGAGGAAGACAAGTCGTGTCTGTCTCTATACAGTGGTCAATCCCCATGCTGAACC  
CTGTGATCTACAGCTTAAGAAACAAGATGTAAAAAGCGCCTTCAGAAAGGTCGCTAGGA  
GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

**AOLFR25 sequences:**

55 METGNLTWVSDFVFLGLSQTRFLQRFLLMFLVYITTVMGNILIITVTSDSLHPTMYFLLRN  
LAVLDLFCSSVTAPKMLVDLLSEKKTISYQGCMMQIFFHFLGGAMVFLSVMAFDRLLIAISRL  
RYVTVMNTQLWGLVYATWVGFFVHSIVQALMLPLPCGPNILDNFYCDVPQVRLACTDT

SLLEFLKISNSGLLDVVWFLLMSYLFILVMLRSHPGEARRKAASCTCTTHIIVSMIFVPSIY  
ARPFPTFPMKDLVSIGHTVMTMLNPMIYTLRNQDMQAAVRLGRHRLV (SEQ ID NO: 47)

5 ATGGAACACAGGGAACCTCACGTGGGTATCAGACTTGTCTTCTGGGGCTCTCGCAGACTC  
GGGAGCTCCAGCGTTTCTCTTCTAATGTCTCTGTTGTCTACATCACCAGTGTATGGGA  
AACATCTTATCATCATCACAGTGACCTCTGATTCCAGCTCCACACACCCATGACTTCT  
GCTCCGAACCTCGCTGCTCTAGACCTCTGTTCTCTCAGTCACTGCTCCCAAAATGCTAG  
TGGACCTCTCTCTGAGAAGAAAACCATCTCTTACCAGGCTGCATGGGTGAGATCTCTCT  
CTTCCACTTTTGGGAGGTGCCATGGTCTTCTCTCTCAGTGATGGCCTTTGACCGCCTCA  
10 TTGCCATCTCCGGGCCCTCCGCTATGTCAACGCTCATGAACACTCAGCTCTGGGTGGGGCT  
GGTGGTAGCCACCTGGGTGGGAGGCTTTGCCACTCTATTGTCCAGCTGGGTCTGATGCTC  
CCACTGCCCTCTGTGGGCCCAACATTTGGATAACTTCTACTGTGATGTTCCCAAGTACT  
GAGACTTGCCTGCACCTGACACCTCACTGTGGAGTCTCTCAAGATCTCCAACAGTGGGCTG  
CTGGATCTGCTGTGTTCTTCTCTCTCTGATGTCTACTTATTCACTCTGGTGATGCTGAG  
15 GTGACATCCAGGAGGCAAGAAGGAAGGACGCTTCCACTGCACACCCAGCATCATGTG  
GGTTTCCATGATCTTGGTCCAAAGCATTTACCTCTATGCCCGGCCCTTCACTCCATTCCTA  
TGGACAAGCTGTGTCCATCGGCCACACAGTCATGACCCCCATGCTCAACCCCATGATCTA  
TACCCTGAGGAACACAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACCGGCTGGT  
TTGA (SEQ ID NO: 48)

20

**AOLFR26 sequences:**

MAAKNSSVTEFIEGLTHQPLRIPLFFLFGFYTVTVVGNLGLITLIGLNSHLHTPMYFFLNL  
LIDFCSTTTPKMLMSFVSRKNISFTGCMTQLFFCFVVSSEFILSAMAYDRYVAICNPLLYT  
VTMSQCVCLLLLGAYGMGFAGAMAHTGSIMNLTFCADNLVNHFMCDILPLLELSCNSSYM  
25 ELVVFIIVAVDVGMPIVTVFISYALILSLHNSSTEGRSKAFTSCSHIIVSLFFGSGAFMYLKP  
LSILEPQGVKSSLFYTIIVPVLNPLIYSLRNKDKVALRRLTGRKIFS (SEQ ID NO: 49)

ATGCGAGCAAAAACCTCTCTGTGACAGAGTTTATCTCGAAGGCTTAACCCACCAGCCGG  
GACTCGGGATCCCCCTCTTCTCTGTTTCTGGGTTTCTACACGGTCACCGTGGTGGGGAA  
30 CCTGGGCTTGATAACCTGTGATGGGCTGAACCTCTCACTGCACACTCCCATGTACTTCTC  
TTTTAACCTCTCTTTAATAGATTCTGTTTCTCCACTACCATCACTCCCAAAATGCTGATG  
AGTTTGTCTCAAGGAAGAACATATTCTCTCACAGGCTGTATGACTCAGCTCTTCTCTT  
CTGCTCTTTGTGCTCTCTGAGTCTTCACTCTGTCAGCGATGGCGATGACCGCTACGTTG  
CCATCTGTAACCCCATGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTGCTCTTTT  
35 TTGGTGCTATGAGATGGGGTTTGTCTGGGCCATGGCCACACAGGAAGCATAATGAAC  
CTGACCTTCTGTGCTGACAACTTGTCAATCATTTGATGTGATCATCTCTCTCTCTTGA  
GCTCTCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTTGGTGGCTGTGAC  
GTTGGAATGCCATGTGCTACTGCTTTATTCTTATGCCCTCATCTCTCCAGCATTTCTACA  
CAACAGTTCTACAGAAGGCAGGTCCAAAGCCCTTTAGTACTTGCACTTCCACATAATTGTA  
40 GTTCTCTTTTCTTGGTCTGCTGCTTCTATGATCTCAAAACCCCTTCCACTCTGCCCTC  
GAGCAAGGGAAGTGTCTCCCTGTTCTATACCATAATAGTCCCGTGTAAACCCATTAA  
TCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCTGAGGAGAACTTTGGGCAGAAAA  
TCTTTCTTAA (SEQ ID NO: 50)

**AOLFR27 sequences:**

MPNQNSYSEFNLFSGSAFPQHLLPILFLYLLMFLFTLLGNLLIMATIWIHRLHTPMYFLCTL  
SVSEILFTVAITPRMLADLLSTHSHITFVACANQMFFSMFGFTHSFLLLVMGYDRYVAICHLR  
YNVLMSPRDCAHLVACTWAGGSMVGMVMVITIVFHLTCFSGSNVHHFFCHVLVSLKLACENKT  
SSVIMGVMLVCVTALIGCLFLIILSVFIVAAILRIPSAEGRHKTFSTCVSHLTVVTVHYSFIFY  
50 LKPKGLHSMYSDALMATTYTVTFPLSPIHSLRNKELKNAINKNFYRKFPCPPSS (SEQ ID NO:  
51)

ATGCCATGTCAGAACTATAGCATCATATCTGAATTTAAACCTCTTTGGCTTCTCAGCCTTCCC  
CCAGCACTCTCTGCCCATCTTGTCTCTGCTGTACTCTGATGTTCTCTGTTCATCTGCTGG  
55 GCAACCTCTCATCATGCCCAACCTGGAATGAACACAGACTCCACACACCATGTACTCT  
CTTCTGTGTCACCTCTCCGTCTCTGAGATTCTGTTCACTGTTGCCATCACCCCTCGCATGC

TGGCTGATCTGCTTTCCACCCATCATTCATCACCTTTTGTGGCTTGTGCCAACCCAGATGTTCT  
 TTCTCCTTCATGTTTGGCTTCACTCACTCCTTCTCTCTGGTCACTGGGCTATGATCGCTA  
 TTGGGCCATCTGCCACCCACTGCGTTACAATGTGCTCATGAGCCCCGTGACTGTGCCCAT  
 CTTGTGGCCTGTACCTGGGCTGGTGGCTCAGTCATGGGGATGATGGTGACAACGATAGTTT  
 5 TCCACCTCACTTTCTGTGGGTCTAAATGTGATCCACCATTTTTCTGTGTCATGTGCTTTCCCTCT  
 TGAAGTTGGCCTGTGAAAACAAGACATCATCTGTCACTATGGGTGTGATGCTGGTGTGTGT  
 CACAGCCCTGATAGGCTGTTTATTCCTCATCATCTCTCTATGTCTTCAATTGTGGCTGCCA  
 TCTTGAGGATTCCTCTGCGGAAGGCCGCGCACAGAATTTTCTACGTGTGATATCCCACT  
 CACTGGGTGGTGTGACGCACTATAGTTTGTCTCTTTATCTACTCAAGGCCAAGGGCCTCC  
 10 ATTCTATGTACAGTGAAGCCTTGTATGGCCACCCTATACCTGTCTTACCCCCCTTCTTATGC  
 CCAATCATTTTACGCTTAAGGAACAAGGAGTGAAGAATAAAAACTTTTACA  
 GAAAATTCTGTCTCCAAGTTCCTGA (SEQ ID NO: 52)

# **AOLFR28 sequences:**

15 MPNFTDVTFTLLGLTCRQELQVLFVVFLAVYMITLLGNIGMILISISPQLQSPMYFFLSHLFS  
 ADVCFSSNVPKMLENLLSETKTISYVGCLVQCYFFIAVVHVYVILAVMAFDRYMAGCXPLL  
 YGSKMSRIVCVRLISVXYXYGFSVSLICTLWTYGLYFCGNFEINHFYCADPPLLIQACRGVHIKE  
 ITMIVAGINFTYLSVLIVSYTLIVVAVLRMRSDGRRKAFSTCGSHLTAVSMFYGTPIFMYLR  
 RPTESVEQKGMVAVFYTTVPMNLNPMIYSLRNKDVKEAVNKAITKTYVRQ (SEQ ID NO: 53)  
 20  
 ATGCCTAATTTACGGATGTGACAGAATTTACTCTCTGGGGCTGACCTGTCGTGAGGAGC  
 TACAGGTTCCTTTTTTGTGGTGTCTTAGCGGTTTACATGATCACTCTGTTGGGAAATATT  
 GGTATGATCATTTTGATTAGCATCAGTCCTCAGCTTCAGAGTCCCATGTACTTTTTCTGAG  
 TCATCTGCTCTTTTGGCGGAGTGTGCTTCTCTCCAACGTTACCCCCAAAATGCTGGAAAACT  
 25 TATTATCAGAGACAAACCATTTCCTATGTGGGATGCTTGGTGCACTGTCTACTTTTCAT  
 TGCCGTTGTGCCAGTGAAGGCTCTATATCTGGCTGTGATGGCCTTTGACAGGTACATCGCC  
 GGCTGCAANCCTCTGCTTTATGGCAGTAAAATGTCTAGGACTGTGTGTGTTCGGCTCATCT  
 CTGTGNNTATGNNATGATTTCTCTGTCAGCCTAATATGCACACTATGGACTTATGGCTT  
 ATACTCTCTGTGGAACITTTGAAATCAATCACTCTATTGTGCACTATCCCTCTTATCCAGA  
 30 TTGCTGTGGGAGATGCACATCAAGAAATCACAATGATTGTTATTGCTGGAATTAACCT  
 CACATATTCCCTCTCGGTGGTCTCATCTCTCACTCTCATTGTAGTAGCTGTGTCACGCA  
 TGCCTCTGCCGATGGCAGGAGGAAGCGCTTCTCCACCTGTGGGTGCCACTTGACGGCTGT  
 TTCTATGTTTTATGGGACCCCATCTTCATGTATCTCAGGAGACCCCACTGAGGAATCCGTA  
 35 GAGCAGGCAAAATGGTGGCTGTGTTTACACCAAGTAATTCCTATTGTTGAATCCCATGA  
 TCTACAGCTCGAAGAAATAAGGATGTAAAAGAAGCAGTCAACAAAGCAATCACCAAGACAT  
 ATGTGAGGCAGTAA (SEQ ID NO: 54)

# **AOLFR29 sequences:**

40 MMSFAPNASHSPVFLLLGFSRANISYTLFLFLAIYLLTTLGNVTLVLLISWDSRLHSPMYLLR  
 GLSVIDMGLSTVTLPLLALHLSHYPTIPAARCLAQFFFFYAFGVTDLTVIAVMALDRYVAICD  
 PLHYALVMNHQRCACLLALSVMVLSILHMLRVGLVPLCWTGDAGGNVNLPHFFCDHRLPLL  
 ASCSDIHSNELAIFFEAGGFLMLGPCALIVLSYVRIGAAILRLPSAAGRRRAVSTCGSHLTMVGFL  
 YGTICVYFQPPFQNSQYQDMVASVMYTATPLANPFVYSLHNKDVKGALCRLLEWVKYDP  
 (SEQ ID NO: 55)  
 45  
 ATGATGAGCTTTGCCCTAATGCTTCACACTCTCCGGTTTTTTTGTCTCTGGGTCTCGAG  
 AGCTAACATCTCCTACACTCTCCTCTTCTCTCTGTTCTGGCTATTACTGACCAACCATAC  
 TGGGGAAATGTGACACTGGTGTGCTCATCTCTGGGACTCCAGACTGCACTACCCATGTA  
 50 TATCTGCTCTGTGGCCTCTCTGTATAGACATGGGCTATCCACAGTTACACTGCCCCAG  
 TTGCTGGCCCATTTGGTCTCTCATTACCAACCATTCCTGCTGCCCGTCTGTTGGCTCAGTT  
 CTTTCTCTCTATGCAATTTGGGGTTACAGATACACTTGTCAATTGCTGTGATGGCTCTGGATC  
 GCTATGTGGCCATCTGTGACCCCTGCACTATGCTTTTGGTAATGAATACCAACCGGTGTGC  
 CTGCTTACTAGCCTTGAAGCTGGGTGGTGTCCATACTGCACACCATGTTGGCTGTGGGACT  
 GTCTGCTCTCTTGTGACTGGGATGCTGGGGCAACGTTAACTCTCTCACTCTTTTGT  
 55 TGACCAACCGGCCACTCTGCGAGCCTCTGTTCTGACATACACTCTAATGAGCTGGCCATA  
 TTCTTTGAGGGTGGCTTCTTATGCTGGGCCCTGTGCCCTCATTGTACTCTCTATGTCCG

AATTGGGGCCGCTATTCTACGTTTGCCCTTCAGCTGCTGGTCGCCGCCGAGCAGTCTCCACC  
 TGTGGATCCCACTCACCATGGTTGGTTTCTCTACGGCACCATCAITTTGTGTCTACTTCCA  
 GCCTCCCTTCCAGAACTCTCAGTATCAGGACATGGTGGCTTCAGTAATGTATACCTGCCATT  
 ACACCTTTGGCCAACCCATTGTGTATAGCCTCCACAATAAGGATGTCAAGGGTGCACCTCT  
 5 GCAGGCTGCTTGAATGGGTGAAGGTAGACCCCTGA (SEQ ID NO: 56)

# **AOLFR30 sequences:**

MGFLSPMPCRPPTQRRMAAGNHSTVTEFILKGLTKRADLQLPLFLFLGIYLVTVGNLGMIT  
 10 LCLNSQLHTPMYFYFLSNLSLMDLCYSSVITPKMLVNFVSEKNHISYAGCMSQLYFLVLFVIAEC  
 YMLTVMAVYDRYVXXCHPLLNIYIMSHHTCLLLVAVVYAIGLIGSTIETGLMLKLPYCEHLISHY  
 FCDLPLMKLSCSSTYDVEMTVFFSAGFNHIVTSLTVLSYFTLISLLGISTTEGRSKAFSTCSSHL  
 AAVGMFYGSTAFMYLKPSTISSLTQENVASVFYTVTPMLNPLIYSLRNKEVKAAYQKTLRKG  
 LF (SEQ ID NO: 57)

15 ATGGGGTCTTGCTGCCATGCATCCCTGCAGGCCTCCCAACCCAGAGGAGAATGGCTGCAG  
 GAAATCACTCTACAGTGACAGAGTTCACTTCTCAAGGGTTTAACGAAGAGAGCAGACCTCC  
 AGCTCCCCCTCTTTCTCTCTCTCGGGATCTACTTGGTCACCATCGTGGGGAACCTGGGCC  
 ATGATCACTCAATTTTGCTGAACCTTCAGCTGCACACCCCATGTACTACTTTCTCAGCA  
 TCTGTCACTCATGGATCTCTGCTACTCTCCGCTATTACCCCTAAGATGCTGGTGAACCTTG  
 20 TGTCAGAGAAAAACACTATCTCTACGCAGGGTGATGTCACAGCTCTACTCTTCTCTGT  
 TTTTGATTTGCTGATGTTGATGTTACATGCTGACAGTGATGGCTACGACCGCTATGTTGNCNTC  
 TGCCACCCCTTTGCTTTTACAACATCATTAATGTCTCATCACACCTGCCTGCTGCTGGTGGCTGT  
 GGTCTACGCCATCGGACTCATTGGCTCCACAATAGAACTGGCCCTCATGTATAAAGCTGCC  
 TATTGTGAGCACCTCATCAGTCACTACTTCTGTGACATCTCCCTCTCATGAAGCTGTCTCTG  
 25 CTATGACACCTATGATGTTGAGATGACAGTCTCTTTTCGGCTGGATCAACATCATAGTC  
 ACGAGCTTAACAGTCTTGTGTTTCTTACACCTTCACTTCTCTCAGCAGTCTCTCGGCATCAGCAC  
 CACAGAGGGGAGATCCAAAGCCTTCAGCACCTGCCAGCTCCCACTTCGACGCCGTGGGAAT  
 GTTCTATGGATCAACTGCAITTCATGTACTTAAACCCCTCCACAATCAGTTTCTTGAACCCAG  
 GAGAATGTGGCCTCTGTGTTCTACACCAACGGTAATCCCATGTGTAATCCCTAATCTACA  
 30 GCCTGAGGAACAAGGAAGTAAAGGCTGCCGTGCAGAAACCGCTGAGGGGTAACCTGTTT  
 GA (SEQ ID NO: 58)

# **AOLFR31 sequences:**

MGTGNDTTVVEFTLLGLSEDTTVCAILFLVFLGIYVVTLMGNISIIHIRRSHLHTPMYIFLCHL  
 35 AFVDIGYSSSVTPVMLMSFLRKETSLPVAGCVAQLCSVVTFGTAECLLAAAMAYDRYVAICSP  
 LLYSTCMSPGVCHLVGMSYLVGGCVNAWTFIGCLRLHFCGPNKYNHFFCDYSPLKLKACSHDF  
 TEIIPAISGSHIVATVCVIAISYIYLITLKMHSKGRHKAFSTCTSHLTAVLFYGTITFHYVMP  
 KSSYSTDQNKVVSVFYTVTPMLNPLIYSLRNKEIKGALKRELRIKIFS (SEQ ID NO: 59)

40 ATGGGGACTGGAAATGACACCACTGTGGTAGAGTTTACTCTTTTGGGGTTATCTGAGGATA  
 CTACAGTTTGTGCTATTTTATTTCTGTGTTTCTAGGAATTTATGTGTGCACCTTAATGGGT  
 AATATCAGCATAAATGTTATGATCAGAGAAGTCACTCTTCATACACCCATGTACATTT  
 TCCTCTGCATTGTGCTTTGTAGACATTGGGTACTCTCATCAGTCAACCTGTGCATGCTC  
 ATGAGCTTCTCAAGGAAAGAAACCTCTCTCCCTGTGCTGGTGTGTGTGGCCAGCTCTGTT  
 45 CTGTAGTGACGTTTGGTACGGCCGAGTGCTCTCTGCTGGCTGCCATGGCCATGATCGCTAT  
 TGTTGGCCATCTGCTCACCCTGCTCTACTCTACCTGTCATGTCCCTGGAGTCTGCATCATCT  
 TAGTGGGCACTGTCTTACCTACCTGGGTGGATGTGTGAATGCTTGGACATTCATTGGCTGCTATT  
 AAGACTGTCTCTCTGTGGGCCAAATAAAGTCAATCACTTTTCTGTGTGACTATCCACCACTT  
 TGAAGCTTGCTTGTTCCTCATGATTTTACTTTTGAATAATTCAGTACTTCTCTGGATCT  
 50 ATCATGTGTGGCCACTGTGTGTGTATAGCCATATCTCATCATATCTCATACCATCTCT  
 GAAGATGACCTCCCAAGAGGGCCGCCACAAGGCCCTTCTCCACCTGCACCTCCCACTCACT  
 CGAGTCACTCTGTCTATGGGACCATTACCTTCACTTATGTGATGCCCAAGTCAGCTACTC  
 AACTGACCAAGAACAGGTGGTGTCTGTGTTCTACACCGTGGTGATTCATGTGTAACCC  
 CTGATCTACAGCCTCAGGAACAAGGAGATTAAAGGGGCTCTGAAGAGAGACTTGAATA  
 55 AAAATATTTTCTTGA (SEQ ID NO: 60)



**AOLFR32 sequences:**

MNSLKDGNHTALTGFILLGLTDDPILRVILFMILSGNLSIILIRISSQLHHPMYFFLSHLAFADM  
AYSSSVTPNMLVNFLVRNTVSYLGCALQLSAAFFATVECVLLAAMAYDRFVAICSPLLYSTK  
MSTQVSVQLLLVVYIAGFLIAVSYTTSFYLLFCGPNQVNHFFCDFAPLLELSSCSDISVSTVVLFSF  
5 SSGSHYVTVVCVIAVCYIYILJILKMRSTEGHHKAFSTCSHLTVVTLFYGTITFIYVMPNFYST  
DQNKVVSVLYTVVPMNLNPLIYSLRNEIKGALKRELVRKILSHDACYFRTSNNDIT (SEQ ID  
NO: 61)

ATGAATTCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCCTATTGGGCTTAA  
10 CAGATGATCCAATCCTTCGAGTCATCTTCATGATCATCTATCTGGTAATCTCAGCATA  
ATTATICTTATCAGAATTTCTTCTCAGCTCCATCATCTATGTATTTCTTCTGAGCCACTT  
GGCTTTTGCTGACATGGCCTATTCATCTTCTGTCACACCCAACATGCTGTAAACATTCCTGG  
TGGAGAGAAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGGTTCAGCGGGTTTCTT  
15 TGCAACAGTCGAATGCGTCTCTTGGCTGCCATGGCCTATGACCGCTTTGTGGCAATTGCA  
AGTCCACTGCTTTATTCAACCAAAAATGTCCACACAAGTCAGTGCCAGCTACTCTTAGTAG  
TTTACATAGCTGGTTTTCTCATGTGCTCTCTATACTACTTCCCTCTATTTTTTACTCTTCT  
GTGGACAAATCAAGTCAATCAATTTTTCTGTGATTCGCTCCCTACTTGAACCTCTCTGT  
TCTGATATCAGTGTCTCCACAGTTGTCTCTCATTTTCTTCTGGATCCATCATTGTGGTCAC  
TGTGTGTGTCATAGCCGCTCTGCTACATCTATATCTCATACCACTCTGAAGATGGCGTCCA  
20 CTGAGGGGCCACCAAGGCGCTTCTCCACCTGCCATCTCCCACTCACTGTGGTTACCGTGT  
CTATGGGACCAATTACCTTCATTTATGTGATGCCCAATTTAGCTACTCAACTGACCAAGAAC  
AAGGTGGTGTCTGTGTGTACACAGTGGTGATTCCTCATGTTGAACCCCTGATCTACAGCC  
TCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTGTGAAGAAAATACTTTCTC  
ATGATGCTTGTATTATTAGTAGAACTTCAAAAATGATATTACATAG (SEQ ID NO: 62)

**AOLFR34 sequences:**

MLEGVEHLLLLLLLDVNSKELQSGNQTSVSHFILVGLHHPQLGAPLFLAFLVIYLLTVSGNG  
LIILTVLVDIRLHRPMCLFLCHLSFLDMTISCAIVPKMLAGFLLSRIISFGGCVQLFSFHLGCT  
ECFLYTLMAYDRFLAICADPLHYATIMTHRVNSCLALGTLWGLGIVFLFQTSFVFLRPFPCGNRV  
30 DYIFDCPAMRLRACTAINELVTFADIGFLALTCFMLILTSYGIYVAAILRIPSADGRNRNFS  
CAAHLTVVIVVYVPCFTFIYLRPCSQEPLDGVVAVFYTVITPLLSHYTLCKNKEMKAALQRLGG  
HKEVQPH (SEQ ID NO: 63)

ATGTTAGAGGGTGTGAGCATCTCCTTCTGCTACTTCTTTTGACAGATGTGAACAGCAAGG  
35 AACTGCAAAAGTGGAAACAGACTCTGTGTCTCACTTCACTTTTGGTGGGCGTGACCAACCC  
ACCACAGCTGGGAGCGGCACCTCTTCTTAGCTTTCCTTGTCACTCATCTCCTCACTGTTTCTG  
GAAATGGGCTCATCATCTCTCACTGTCTTAGTGGACATCCGGCTCCATGCTCCCATGTGCTT  
GTTCTGTGTGCACCTCTCCTTCTTGGACATGACCACTTCTGTGCTATGTTGCCCAAGATG  
TGGCTGCCATTTCTCTTGGGTAGTAGGATTAATCTCCTTTGGGGGCTGTGTAATCCAACATTT  
40 TCTTTCCTTTCTGGGCTGTAAGTGTGCTTCTTACACATCATGCGCTTATGACCGTTT  
CCTTGCCATTTGTAAGCCCTTACACTATGCTACCATCATGACCCACAGAGTCTGTAACCTCCC  
TGGCTTTTAGGCACCTGTGGGAGGACTATCCTACTTCTTTCCAAACAAGTTTGTATTT  
CCGGCTGCCCTTCTGTGGCCCAATCGGGTCGACTACATCTTCTGTGACATTCTCGCCATGC  
TCTGCTCATGCTGCGCGATACGCGCATCAACGAGCTGGTCACTTTTCGACAGATTGGCTT  
45 CCGTGGCCTCACCTGCTTCATGCTCATCTCACTTCTATGGCTATATTGTAGCTGACCTATC  
TGGCAATTCCTGAGAGATGGGCGCGCAATGCCTTCTCCACTTGTGCTGCGCCACCTCAC  
TGTGTGATTTGTTACTATGTGCCCTGCACCTTCAATTAACCTCGCGCTTGTTCACAGGAGC  
CCCTGGATGGGGTGGTAGCTGTCTTTACACTGTGATCACTCCCTTGTCTTAACCTCATCATC  
TACACACTGTGCAACAAGAAATGAAGGCAGATTACAGAGGCTAGGGGGCCACAAGGAA  
50 GTGACGCTCACTGA (SEQ ID NO: 64)

**AOLFR35 sequences:**

MEPLNRTEVSEFFLKGFSGYPALEHLLFPLCSAMYLVTLNGNTAIMAVSVLDIHLHTPVYFFLG  
NLSTLDICYTTPFVPLMLVHLLSSRKTIISFAVCAIQMCLSLSTGSTECLLLAITAYDRYLAICQPL  
55 RYHVLMSHRLCVLLMGAAWVLCLLKSVTENVISMIRLPFCGHVVSHTFKILAVLKLACGNT  
SVSEDFLLAGSILLVPVLAFLICLSYLLILATILRVPSAARCKAFSTCLAHLAVLLFYGTIIFMY

LPKPSKEAHISDEVFTVLYAMVTTMLNPTIYSLRNKEVKEAARKVWGRSRASR (SEQ ID NO: 65)

5 ATGGAGCCGCTCAACAGAACAGAGGTGTCCGAGTCTTTCTGAAAGGATTTTCTGGCTACC  
CAGCCCTGGAGCATCTGCTCTTCCCTCTGTCTCAGCCATGTACTGGTGACCCCTCTGGG  
GAACACAGCCATCATGCGCGGTGAGCGTGCTAGATATCCACCTGCACACGCCCGTGTACTTC  
TTCTCTGGGCAACCTTCTACCCCTGGACATCTGCTACACGCCACCTTTGTGCTCTGTATGCT  
GGTCCACCTCTGTCTATCCCGGAAGACCATCTCCCTTTGCTGTCTGTGCCATCCAGATGTGTCT  
10 TGAGCCTGTCCACGGGGTCCACGGAGTGCTGCTACTGGCCATCAGCGGCTATGACCGCTA  
CTCTGGCCATCTGCCAGCCACTCAGGTACACGTGCTCATGAGCCACCGGCTCTGGGTGCTG  
CTGATGGGAGCTGCTGGTCTCTGCTCTCAAGTCGGTGACTGAGATGGTCACTTCCA  
TGAGGCTGCCCTCTCTGTGGCCACACGTGGTCACTCACTCAGTCAAGATCTCGGCAGT  
GCTGAAGCTGGCATGCGGCAACACGTGGTCAGCGAAGACTTCTGCTGGCGGGCTCCAT  
CCTGCTGCTGCCTGTACCCCTGGCATTCTATGCTGCTCTACTGTCTATCTTGCCACCA  
15 TCTGAGGGTGCCCTCGGCCGCCAGGTGCTGCAAAAGCCTTCTCCACCTGCTTGGCACACCT  
GGCTGTAGTGCTGCTTTTCTACGGCACCATCATCTTATGTACTGAAGCCCAAGAGTAAG  
GAAGCCACATCTCTGATGAGGTCTTACAGTCTCTATGCCATGGTCACGCCATGCTGA  
ACCCACCATCTACAGCCTGAGGAACAAGGAGGTGAAGGAGCGGCCAGGAAGGTGTGGG  
GCAGGAGTCGGGCTCCAGGTGA (SEQ ID NO: 66)

20 **AOLFR36 sequences:**  
MYLVTVLRNLSLAVSSDSHPHTPMYFFLSNLCWADIGTFLATVPKMIVDMGSHSKVISYGG  
CLTQMSFLVLFACIVDMFLTVMAYDCFAICRPLHYPIVNPHLCVFFVLVSFFLSLLDSQLHS  
WVILQFTLFFKNVEISNFCVCEPSQLKLASYDSVINSIFIYFDNTMFGLPISGILLSYKIVPSILRIS  
25 SSDGKYAFSAKCHLAVVCLFYGTGTGIVYLTSAVAPLRNGMVASVMYAVVTPMLNPFYIS  
LRNRDIQSALWRVCNKTVESHDLFHPFSCVVEKGQPHSIPTSANPAP (SEQ ID NO: 67)

30 ATGTATCTGGTCACGGTGCTGAGGAACTGCTCAGCATCCTGGCTGTCAGCTCTGACTCCC  
ATCCCCACACACCCATGTACTTCTTCTCTCCAACTGCTGCTGGGCTGACATCGGTTTACCT  
TTGGCCACGGTTCCCAAAGATGATTGGACATGGGGTCGCATAGCAAAGTCATCTTTATG  
GGGGCTGCCTGACACAGATGTCTTCTTGGTACTTTTGTGATGTATAGTAGACATGTTCTCT  
GACTGTGATGGCTTATGACTGCTTTGTAGCCATCTGTGCGCCTCTGCACTACCCAGTCATC  
GTGAATCTCAACCTCTGTGTCTTCTCGTTTGTGTCTCTTTCTTACCTGAGCTGTGGATTCC  
35 CAGCTGCACAGTGTGGATTGTGTACAAATTCACCTTCTTCAAGAAATGTGGAAATCTCTAATT  
TTGTCTGTGAGCCATCTCAACTTCTCAAGCTTGCCCTTATGACAGCGTCATCAATAGCATA  
TTCATATATTTGATAATACTATGTTTGGTTTCTTCCCATTTACAGGATCCCTTTTGTCTTAC  
TATAAAATTTGCCCTCACTTCAAGGATTTATCATCAGATGGGAAGTACAAAGCCTTCT  
CAGCTGTGGCTGTCACTGGCAGTTGTTTGTCTTATTTATGGAACAGGCATTTGGCGTGA  
CCTGACTTCACTGTGGCACCAACCTCAGGAATGGTATGGTGCGTCAGTGATGACGCT  
40 TGTGTCAACCCCATGTGAAACCTTTTATCTACAGCCTGAGAAACAGGGACATCTCAAAGTG  
CCCTGTGGAGGGTGTGCAACAAAACAGTCAATCTATGATCTGTTCCATCTCTTTTCTGT  
TGTGGTTGAGAAAGGGCAACCACTTCAATCCCTACATCTGCAAACTCTGCCCTTAG  
(SEQ ID NO: 68)

45 **AOLFR37 sequences:**  
MEKANETSPVMGFVLLRLSAHPELEKTTFFVILLMYLVILLGNVILVLTILDRLHTPMYFFLG  
NLSFLDICTSSVPLVDSFLTPOETISFSACAVQMALSFAMAGTECLLLSMAFDRYVAICNP  
LRYSVIMSKAAYMPMAASSWAIGGAASVVHTSLAIQLPFGCGDNVINHFTCEILAVLKLACADIS  
INVISMEVNTNVLFGVPLVFISFSYVFIITILRIPSAEGRKKVFTSCAHLTVVVFYGTLLFFMYG  
50 KPKSKDSMGADKEDLSKLPLFYGVVTPMLNPIYSIRNKDVCAAVRRLLRPKGFTQ (SEQ ID  
NO: 69)

55 ATGAAAAAGCCAATGAGACCTCCCTGTGATGGGGTTCGTTCTCTGAGGCTCTCTGCC  
ACCAAGAGCTGGAAAGACATCTCTCGTGCTCATCTGCTGATGATGACCTCGTGTACTCGTGT  
GGGCAATGGGGTCTCTATCTCGTGGTGACCATCTTGACTCCGCGCTGCACACGCCATGTAC  
TTCTTCTAGGGAACCTCTCTCTTCTGGACATCTGCTTCACTACCTCTCAGTCCCCTGTT

CCTGGACAGCTTTTGTACTCCCCAGGAAACCATCTCCTTCTCAGCCTGTGCTGTGCAGATG  
 GCACCTCTCCTTTGCCATGGCAGGAACAGAGTGCTTGCTCCTGAGCATGATGGCATTGTGATC  
 GCTATGTGGCCATCTGCAACCCCTTAGGTACTCCGTGATCATGAGCAAGGCTGCTACAT  
 GCCCATGGCTGCCAGCTCTGGGCTATTGGTGGTGTCTGCTCCGTGGTACACACATCCTTG  
 5 GCAATTTCAGCTGCCCTCTGTGGAGACAATGTCATCAACCCTTACCTGTGAGATTCTGG  
 CTGTTCTCAAAGTTGGCCTGTGCTGACATTTCCATCAATGTGATCAGCATGGAGGTGACGAA  
 TGTGATCTTCTAGGAGTCCCGGTTCTGTTCTATCTCTTCTCCATGTCTTCTCATCAACCA  
 CCATCTCAGGATCCCTCAGCTGAGGGGAGGAAAAAGGTCTTCTCCACCTGCTCTGCCCA  
 CCTCACCGTGGTGTGCTCTTCTACGGGACCTTATCTTCATGTATGGGAAGCACTAAGCT  
 10 AAGGACTCCATGGGAGCAGACAAAGAGGATCTTTCAGACAACTCATCCCCCTTTCTATG  
 GGGTGGTGACCCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGATGTGAAGG  
 CTGCTGTGAGGAGACTGTGAGACCAAAAGGCTTCACTCAGTGA (SEQ ID NO: 70)

#### AOLFR38 sequences:

15 MYLVTVLRNLLILAVSSDSLHPTMCFFLSNLCWADIGFTSAMVPKIMVDMQSHSRVISYAGC  
 LTQMSFFVLVACIEDMLLTVMAYDRFVAICHPHYVPMINPHLGVFLVLVSFFLLSLLDSQLHSW  
 IVLQITFFKNVEISNFCVDPQSLNLCDSVINSIFILYDSIMFGFLPISGILLSYANNVPSILRISS  
 SDRKSKAFSTCGSHLAVVCLFYGFTGIGVYLTSAVSPPRNGVVASVMYAVVTPMLNPFYISLR  
 NRDIQSALWRLRSRTVESHDLLSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)  
 20  
 ATGTACCTGGTCACGGTGTGCTGAGGAACCTGCTCATCATCTGGCTGTACGCTCTGACTCCC  
 ACCTCCACACCCCATGTGCTTCTTCTCTCCAACTGTGCTGGGCTGACATCGGTTTCAAC  
 TCGGCCATGGTTCCTCCAAAGATGATTGTGGACATGCAGTCGATAGCAGATCATCTTATG  
 CGGGCTGCCTGACACAGATGCTTCTTCTTGTCTTTTGTGATATAGAAGACATGCTCCTG  
 25 ACAGTGAATGGCCTATGACCGATTGTGGCCATCTGTCAACCCCTGCACCTACCCAGTCATA  
 TGAATCTCACTTGGTGTCTCTTAGTTTGGTGCTTTTCTCAGCCTGTTGGATTCC  
 CAGCTGCACAGTTGGATTGTGTTACAATTCAACCTCTTCAAGAAATGTGGAAATCTCAATT  
 TTGCTGTGACCCATCTCAACTTCTCAACCTTGCTGTCTGTGACAGTGTATCAATAGCATA  
 30 TTATATATTTAGATAGATTATGTTTGGTTTCTTCTCCCATTTCAAGGATCTTTTGTCTTAC  
 GCTAACAAATGTCCCTCCATTCTAAGAATTTATCATCAGATAGGAAGTCTAAAGCCTTCT  
 CCACCTGTGGCTCTACCTGGCAGTGTGTTGCTATTTTATGGAACAGGCATTGGCGTGTA  
 CTTGACTTCACTGTGTACCAACCCCCAGGAATGGTGTGGTGGCATCAGTGATGTACGCT  
 GTGGTCAACCCCATGCTGAACCTTTTATCATCAGCCTGAGAAATAGGACATTTCAAAAGTG  
 35 CCGTGTGGAGGCTGCGCAGCAGAACAGTCAATCTCATGTCTGTTATCTCAAGATCTGCT  
 CCATCTGTTTCTGTGTGGGTGAGAAAGGTCAACCATTA (SEQ ID NO: 72)

#### AOLFR39 sequences:

MGVKNHSTVTEFLLSLTEQAEQLPLFLGIYTVTVGNLSMISIIRLNRLHTPMYYFLSS  
 LSLDFCYSSVITPKMLSGFLCRDRSISYSGCMIQLFFVCVISECYMLAAMACDRYVAICSP  
 40 LYRVIMSPRVCSLLVAAVFSVGFTDAVHGGCILRLSFCGSNIKHXYFCDIVPLIKLSCSYIDEL  
 LIFVIGFENMVATSLTIISYAFILTSILRIHKKGRKAFSTCSSHLTAVLMFYGSLMSMYLKPAS  
 SSSLTQEKVSSVFYTTVILMLNPLIYSIRNNEVRNALMKLLRRKILSLPG (SEQ ID NO: 73)  
 45  
 ATGGGTGTAAAAAACCATTCACAGTGACTGAGTTTCTTCTTTCAGGATTAACCTGAACAAG  
 CAGAGCTTCAGCTGCCCTCTTCTGCTCTTCTAGGAATTTACAGATTACTGTGGTGGG  
 AAACCTCAGCATGATCTCAATTTATAGGCTGAATCGTCAACTTCATACCCCATGTACTAT  
 TTCTGAGTAGTTGTCTTTTATAGATTCTGTCTATCTGTCTATACCCCTAAATGCT  
 ATCAGGGTTTTATGACAGAGATAGATCCATCTCTCTTCTGGATGCATGATTCAGCTGTTTT  
 TTTCTGTGTTTGTGTATTTCTGAATGCTACATGCTGGCAGCCATGGCTGCGATCGCTAC  
 50 GTGGCCATCTGCAGCCCACTGCTCTACAGGGTCTCATGTCCCTGAGGGTGTCTTCTCTG  
 TGGTGGCTGCTGTCTTCTCAGTAGGTTTCACTGATGCTGTGATCCATGGAGGTTGCTATAC  
 CAGGTTGTCTTTCTGTGGATCAAAACATCAATAACATTATTTCTGTGACATTGTCCCTCTTA  
 TAAACTCTCTGCTCCAGCACTTATATTGATGAGCTTTTGATTTTGTCAATGGTGGATT  
 AACATGGTGGCCACAGCCTAACATCATTTTTCATAGCTTTATCTCCAGCAGCATCCT  
 55 CGCATCTGACCTCAAAAAGGGCAGGTGCAAAAGCGTTTAGCACTGTAGCTCCCACTGACA  
 GCTGTTCTTAATGTTTATAGGGTCTGATGTCCATGTATCTCAAAACCTGCTTCTAGCAGTTC

ACTCACCCAGGAGAAAGTATCCTCAGTATTTTATACCACTGTGATTCTCATGTTGAATCCC  
TTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAAACATTTAAGAAGA  
AAAATATCTTTATCTCCAGGATAA (SEQ ID NO: 74)

5 **AOLFR40 sequences:**

MSNATLLTAFILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNS  
FIDMWFSTVTVPKMLMTLVSPSGRTISFHSVCVQLYFFHFLGSTEFCFLYTVMSYDRYLAISYPL  
RYTNMMTGRSCALLATGTWLSGSLHSAVQTLTFHLPYCGPNQIQHYFCDAPPILKLACADTS  
ANEMVIFVNI GLVASGCFVLIVLSYVSIVCSILIRITSEGRHRAFQTCASHCIVVLCTFFGPGLFIYL  
10 RPSRDLHGUVAVFYTTLTPLNPNVYTLRNKEVKKALLKLKNGSVFAQGE (SEQ ID NO:  
75)

ATGTCCAACGCCACCCTACTGACAGCGTTTCATCTCACGGGCTTCCCCATGCCCGAGGGC  
15 TGGACGCCCCCTCTTTGGAATCTCTCGTGGTGTACGTGCTCACTGTGCTGGGGAACCT  
CCTCATCTCGTGGTGATCAGGGTGGATTCTCACCTCCACACCCCACTGACTACTTCTCA  
CCAACCTGTCTTATTGACATGTGGTCTCCACTGTACGGTGCCCAAAATGCTGATGAC  
CTTGGTGTCCCAAGCGGCAAGGACTATCTCTTCCACAGCTGCGTGGCTCAGCTCTATTTT  
TCCACTTCTCTGGGAGCACCGAGTGTTCCTCTACACAGTCATGTCTTATGATCGCTACTC  
20 GGCATCAGTATACCGCTCAGGTACACCAACATGATGACTGGGCGCTCGTGTGCCCTCTCTG  
GCCACGGGCACCTTGGCTCAGTGGCTCTCTGCACTCTGCTGCAGACCATATTGACTTTC  
ATTGTCCCTACTGTGGACCAACAGATCCAGCACTACTTGTGACGCGACCGCCATCCT  
GAAACTGGCTGTGACAGACACCTCAGCCAACGAGATGGTCACTTTGTGAATATTGGGCTA  
GTGGCTCTGGGCTGCTTTGTCTGATAGTGCTGTCTATGTCTCATCGTCTGTTCATCCT  
25 GCGGATCCGCACTCAGAGGGGAGGCACAGAGCCTTTACAGACCTGTGCTCCCACTGTATC  
GTGGTCTTTGTCTCTTTGGCCCTGGTCTTTTCAATTTACCTGAGGCGAGGCTCCAGGAGCG  
CTTGATCGGGGTGTGGCCCTTTTCTACACCAGCTGACTCTCTTTTCAACCCCTGTGTGT  
ACACCTTGAGAAACAAGGAGGTAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTGAGTAT  
TTGCTCAGGGTGAATAG (SEQ ID NO: 76)

30 **AOLFR41 sequences:**

MPNENWTQVTSFVLGFPSSHLIQFLVFLGLMVTVIVTATGKLLIIVLSWIDQRLHIQMYFFLRN  
FSLELLLVTVVVPKMLVVLITGDHTISFVSCIIQSYLYFFLGTTFDFFLLAVMSLDRLYLAI RPLR  
YETLMNGHVCQSLVASWLAGFLWVLCPTVLMASLPFCGPNGIDHFFRDSWPLRLSCGDTH  
LLKLVAFMLSTLVLLGSLALTSVSYACILATVLRAPTAERKRAFSTCASHLTVVVIHGSIFLY  
35 IRMSEAQSKLLNKGASVLSCTIPLNPFIFLRNDKVQQALREALGWPRLTAVMKLRVTSQRK  
(SEQ ID NO: 77)

ATGAACCCCTGAAAACCTGGACTCAGGTAACAAGCTTTGTCTTCTGGGTTTCCCCAGTAGCC  
40 ACCTCATACAGTTCCTGGTGTCTCTGGGGTAAATGGTGACCTACATTGTAACAGCCACAGC  
CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACGCCCTGCACATACAGATGACTTC  
TTCTCGGGAATTTCTCTTCTGGAGCTGTGCTGGTAACTGTTGTGGTTCCTCAAGATGCT  
TGTGCTCATCTCAGCGGGGATCACACCATCTCATTGTGAGCTGCATCATCAGTCTTACC  
TCTACTTTCTTAGGCACCACTGACTTCTTCTTGGCCGTGATGCTCTGGATCGTTAC  
45 CTGGCAATCTGCCGACCACTCCGCTATGAGACCTGATGAATGGCCATGTCTGTTCACCA  
TAGTGTGCGGCTCTGCTAGCTGGATTCTCTGGGTCCTTTGGCCCACTGTCTTGGGCGC  
AGCCTGCCCTTCTGTGGCCCAATGGTATTGACCACTTCTTTCGTGACAGTTGGCCCTTGCT  
CAGGCTTTCTGTGGGGACACCCACCTGCTGAAACCTGGTGGCTTTTCATGCTCTCTACGTT  
GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTTCTTATGCTGCATCTGCTGCTGCTGCT  
50 CAGGCGCCCTACAGCTGCTGAGCGAAGGAAGCGTTTCCACTTGGCCTCGCATCTTACA  
GTGGTGGCTCATCTATGGCAGTTCATCTTCTCTACATTGATGTCAGAGGCTCAGTC  
CAAACCTGCTCAACAAGGTCCTCGTCTGAGCTGCATCATCACACCCCTTTGAACCCA  
TTCATCTTCACTCTCCGCAATGACAAGGTGACGAAGCACTGAGAGAAGCCTTGGGGTGGC  
CCAGGCTCACTGCTGTGATGAAACTAGGAGGTACAAGTCAAAGGAAATGA (SEQ ID NO:  
78)

55

**AOLFR42 sequences:**

- MNPANHSQVAGFVLLGLSQVWELRFVFFTVFSVYFMTVVGNLLIVVIVTSDPHLHTTMYFLL  
GNLSFLDFCYSSITAPRMLVLDLSGNPTISFGGCLTQLFFHHFIGGKIQLLTVMAVYDRYIAISOPL  
HYTLIMNQTVCALLMAASWVGGFIHSIVQIALTIQLPFCGPDKLDNFYCDVPQLIKLACTDTFV  
LELLMYSNNGLVTLMLCFLVLLGSY TALLVMLRSHSREGRSKALSTCASHIAVVTLIFVPCIVVY  
TRPFRITPMDKAVSVLYTIVTPMLNPAIYTLRNKEVIMAMKKLWRRKKDPIGLEHRPLH  
(SEQ ID NO: 79)
- 10 ATGAATCCAGCAAATCATTCCTCCAGGTGGCAGGATTTGTTCTACTGGGGCTCTCTCAGGTTT  
GGGAGCTTCGGTGTGTGTTTCTCTCACTGTTTTCTCTGCTGTGTATTTATGACTGTAGTGGGA  
AACTCTTCTATTGTGGTCATAGTGACCTCCGACCCACACCTGCACACAACCATGTATTTTCT  
CTTGGGCAATCTTCTTCTCTGGACTTTTGCTACTCTTCCATCACAGCACCTAGGATGCTGG  
TTGACTTGCTCTCAGGCAACCC TACCATTCTCTTGGTGGATGCCTGACTCAACTCTCTCTTC  
TTCCACTTCATTGGAGGCATCAAGATCTCTCTGCTGACTGTGATGGCGTATGACCGCTACA  
15 TTGCCATTTCCAGCCCCCTGCCTACACGCTCAATTATGAATCAGACTGTCTGTGCACTCCTT  
ATGGCAGCCTCTGGTGGGGGGCTTCATCCACTCCATAGTACAGATTGCATTGACTATCC  
AGCTGCCATTCTGGGGCTGACAAGCTGGACAACCTTTATTGTGATGTGGCTCAGCTGAT  
CAAAATGGCGCTGCACAGATACCTTTGTCTTAGAGCTTTTAAATGGTGTCTAACAAATGGCGT  
GTGACCTGATGTGTTTCTGTGTCTCTGGGATCGTACACAGCATGCTAGTCATGCTCC  
20 GAAGCCACTCAGGGAGGCCGACAGCAAGGCCCTGTCTACCTGTGCTCTACATTTGCTGT  
GGTGACCTTAATCTTTGTGCTTGCATCTACGCTCTATACAAGGCCCTTTTCGGACATCCCCA  
TGGACAAGGCCGTCTGTGCTATACACAATTTGACCCCATGTGTAATCTCTGGCATCTA  
TACCCTGAGAAACAAGGAAGTATCATGGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG  
ACCTATTGGTCCCCCTGGAGCACAGACCTTACATTAG (SEQ ID NO: 80)
- 25

**AOLFR43 sequences:**

- MQKQLLVPIATSNGLNVHAAFYLLVGIPLGPTIHFWLAFPLCFMYALATLGNLTIVLIIRVE  
RRLHEPMYLFAMLSITIDLVLSSITMPKMASLFLMGIEIEFNICLAQMFLIHLSAVESAVILLA  
MAFDRFAICHPLRHASVLTGCTVAKIGLSALTRGFVFFFLPFLIKWLISYQCQTHTVTSHFLHQ  
30 DIMKLSCTDTRNVNVVLIIFLHLSVYMGVDSFLRIGFYLILWAVLELSSRLAKAFNTCISHLCAV  
LVFVYPLIGLSVVHRLGGPTSLHVVMMANTYLLLPVNVNPLVYGAKTKEICSRVLCMFSQGGK  
(SEQ ID NO: 81)
- 35 ATGCAGAAGCCCCAGCTCTTGGTCCCTATCATAGCCACTTCAAATGAAAATCTGGTCCAGC  
CAGCATACTCTCTTTGGTGGGTATCCCTGGCCTGGGGCTACCATACACTTTTGGCTGGCT  
TTCCCATGTGTTTATGTATGCTTGGCCACCCCTGGGTAACCTGACCATTGTCTCTATCAT  
TCGTGTGGAGAGGCCGACTGCATGAGCCCATGTACCTCTCTCTGGCCATGCTTTCCCATAT  
GACCTAGTCTCTCTCTATACCATGCCCCAAGATGGCCAGCTCTTTCTGATGGGCATCCA  
GGAGACTCGAGTTCAACATTTGCCTGGCCAGATGTCTCTATCATGCTCTGTGAGCCGTG  
40 GAGTCAGCTGCTGCTGGCCATGGCTTTTGACCGCTTTGTGGCATTGTGCCACCCATTGC  
GCCATGCTTCTGTGCTGACAGGGTGTACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG  
GGGGTTTGATTTCTCTTCCACTGCCCTTCATCCTCAAGTGGTGTCTCATGTCACCAACAC  
ATACCTGCACACACTCTCTGTCTGCACCAAGATATTATGAAGCTGTCTGTACTGACAC  
CAGGGTCAATGTGGTTTATGGACTCTCATCATCTCTCATGCTGGGTCTGCTCTCGGAGGCA  
45 TCATTGGCTCTCATATATCTCATCTCTGTGGCTGTGAGCTGTCTCTCGGAGGCA  
GCACCAAGGCTTTCAACACCTGCATCTCCACCTCTGTGCTGTCTGGTCTCTATGTACC  
CCTCATGGGCTCTCGGTGGTGCATAGGCTGGGTGCTCCACCTCCCTCTCATGTGGTT  
ATGGCTAATACCTACTGTGCTGCTACCACTGTAGTCAACCCCTTGTCTATGGAGCCAAGA  
CCAAAGAGATCTGTTCAAGGGTCTCTGTATGTTCTCACAAGGTGGCAAGTGA (SEQ ID  
50 NO: 82)

**AOLFR44 sequences:**

- MSSCNFTHATFVLIGIPLEKAHFVWGFLLSMYVAMFGNCIVVFIVRTERSLHAPMYLFLC  
MLAAIDLALSTSMPLKIALWFSDSREISFEACLQMFHIALSAIESTILLAMAFDRYVAICHPL  
55 RHAADVNNVTVAQIGIVAVVRGSLFFFLPLLIIKRLAFCHSNVLSSHVCVHQDVMKLAYDITLP  
NVVYGLTAILVMGVDMFISLYFLIIRTVLQLPSKSERAKAFGTCVSHGVVLAIFYVPLGLS

VVHRFGNSLHPVRVVMGDIYLLPPVINPHIYGAKTQIRTRVLAMFKISCDKDLQAVGGK  
(SEQ ID NO: 83)

ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCCAGGATTAGAGA  
5 AAGCCCACTTCTGGGTTGGCTTCCCCCTCCTTCCCATGTATGTAGTGGCAATGTTGGAAAC  
TGCACTGTGGTCTTCATCGTAAGGACGGAAACGCGCTGCACGCTCGCATGTACCTCTTTC  
TCTGCATGCTTGCAGCCATTGACCTGGCCTTATCCACATCCACCATTGCCAAGATCCTTGGC  
CTTTTCTGGTTGATTCCCGAGAGATTAGCTTTGAGGCCGTGCTTACCCAGATGTCTTTAT  
10 CCATGCCCTCTCAGCCATTGAATCCACCATCCTGTGCGCATGGCCTTTGACCGTTATGTGG  
TCATCTGCCACCCTGCGCCATGCTGCAGTGCTCAACAATACAGTAACAGCCCAAGATTGG  
CATCGTGGCTGTGGTCCCGGATCCCTCTTTTTCCTCCACTGCCTCTGTGATCAAGCGGC  
TGGCCTCTGCCACTCCAATGTCTCTCGCACCTCTATTGTGTCCACCAGGATGTAATGAA  
GTGTGGCTATGCAGACACTTTGCCAATGTGGTATATGGTCTTACGCCATTCTGCTGGCT  
15 ATGGGCGTGGACGTAATGTTCATCTCCTTGTCTTATTTCTGATAATACGAACGGTCTGCG  
AATCGCCTTCCAAGTCAGAGCGGGGCCAAGGCCTTTGGAACTGTGTGTACACATTTGGTGT  
GGTACTCGGCTCTTATGTGCCACTTATTTGGCCTCTCAGTGGTACACCGCTTTGGAACAGC  
CTTCATCCCATTTGTGCGTGTGTGTCATGGGTGACATCTACCTGCTGCTGCTCTGTCTATCA  
TCCCATCATCTATGGTGCCAAAACCAACAGATCAGAACCGGGTGTGGCTATGTTCAAG  
20 ATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

**AOLFR45 sequences:**

MLPSNITSTHPAVFLVGPGLLEHLHAWISIPFCFAYTLALLGNCTLLFIQADAAALHEPMYFLA  
MLATIDLVSSTLPLKMLAIFWFRDQENFFACLVQMFFLHSFSIMESAVLLAMAFDRYVAICKP  
LHYTTLVLTGSLITKIGMAAVARAVLMTPLPFLRLRFHYCRGPVIAHCYCEHMAVVRACGDT  
25 SFNNIYGLAVAMFSVVDLLFLVILSYVFIQAVLQLASQEARYKAFGTVCVSHIGAILSTYPPVIS  
SVMHRVARHAAPRVHILLAIFYLLFPPMVNPIYGVKTKQIREYVLSLFQRKNM (SEQ ID NO:  
85)

TGGAAACAAGAGGTAATCTTTGCAAGTGGGATAGCACAGGTTGAACTCTAATCATATATA  
30 CTGTAGAAGGTATATATAGAAGGTGAAGAAGCCCTGTAAAAATTGACAAGGAGATTTC  
GGAGCCATGCTTCCCTCTAATATCACTCAACACATCCAGCTGTCTTTTGTGGTAGGAAT  
TCTGGTTTGGAAACACCTGCATGCCTGGATCTCCATCCCTCTCTGCTTTGCTTATACTTGC  
CCCTGCTAGGCAACTGTACCCCTTCTCTCATTAATCCAGGCTGATGCAGCCCTCCATGAAGC  
35 ATGTACCTCTTCTGGCCATGTTGGCAACCAATTGACTTGGTCTTCTTCTACAAACGCTGCC  
CAAAATGCTTGCATATTCTGGTTCAGGGATCAGGAGATCAACTCTTTGGCTGTCTGGTC  
CAGATGTTCTTCTTACTCCTTCTCCATCATGGAAGTACGAGTGTCTGTGGCCATGGCCTT  
TGACCGCTATGTGGCCATCTGCAAGCCATTGCACACTACACGACGGTCTGACTGGGTCCTC  
ATCACCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCT  
TCTGCTCAGACGCTTCCACTACTGCCGAGGCCAGTGATTGCCATTGCTACTGTGAACA  
40 CATGGCTGTGGTAAGGCTGGCGTGTGGGGACCACTAGCTTCAACAATATCATGGCATTGT  
TGGCCATGTTTAGTGTGGTGTGGACCTGCTCTTTGTATCTGTCTTATGTCTTATCTCT  
TCAGGCGATTCTCCAGCTTGCCTCTCAGGAGGCCGCTACAAAGCATTTGGGACATGTGTG  
TCTCATATAGTGCCATCTGTCCACCTACACTCCAGTAGTCATCTTTCAGTCATGCACGG  
TGTAGCCGCGCATGTGCCCCCTCGTGTCCACATACTCTTGTATTTTCTATCTCCTTTTCC  
45 CAGCCATGGTCAATCTATCATATATGGAGTCAAGACCAAGCAGATTGCGAGTAGTGTGCT  
CATCTTATTCAGAGAAAGAACATGTAGATGGATAGTTCTTTTATCCCATGTGCCA  
AGTAATGAGAATGCTGGATTGGGGTTGAGGGGAAAAATCTAAATAGGAAAAATGCAGAGT  
ATCTTTGACAATCTCTAGTATGATAAGGAAAAATGAGGTTTCATTCTCCAGAGATCTACGA  
50 ATGAGCTCAAAACCGAGGAGTGACCTATAGTCTGGTCTGTATAGTAGAGAGGTTTGACCTTCCA  
TTGTGATAGACTATCATATGGCTAAGGAAGACAAACCTCTCAAAGTGGTATGTGAATCTCG  
GGTGAAGACAGTAGGACCTTTATTGGCTGAGATTGGCCAAAACAGCTGAGTG (SEQ ID  
NO: 86)

**AOLFR46 sequences:**

MNIKHCGWHMHTWLNIREDDDSDFKNFQIQGLSGNPHSTSRMYFLCFCTSLLGFKVHWV  
55 SRLIXKLYMASPNDSTAPVSEFLLCFPNFQSWQHWLSLPLSLLFLLAMGANTLLITIQLEAS

LHQPLYLLSLDLLDIVLCLTVIPKVLAIWFDRSISFPACFLQMFIMNSFLTMESCFTMVMVA  
 YDRYYAICHPLRYPSIITDQFVARAVVFIARNAFVSLPVMPLSARLRYCAGNIKNICNSILSVS  
 KLSDDITNLYQFVAGWTLGLSDLLIVISYFSLKVVRLRIKABGAVAKALSTCGSHFILFFS  
 TVLLVLVITNLARKRIPPDPVILLNLHLIPLPALNPVIVGVRTKEIKQGQIQLNLKRL (SEQ ID NO:

5

87)  
 ATGAATATAAAACATTGTGGCTGGCATATGATACATACTTGGTTAAATATAAGGGAGGAT  
 GATGACAGTGATTTTAAAAAAGTTTATGGACAGATACAGGGCCTCAGTGGAAACCCACACT  
 CTACTAGCTCTAGAAATGTACTTTTATGTTTCTGTACTTCTCTACTAGGTTTAAAGGTACAC  
 10 TGGGTCTCCAGATTGATCANGAACTTTACATGGCATCTCCCAACAATGACTCCACTGCCC  
 CAGTCTCTGAATTCCTCCTCATCTGCTTCCCAACTTCCAGAGCTGGCAGCACTGGTTGTCT  
 CTGCCCCCTCAGCCTTCTCTCTCTCTGGCCATGGGAGCTAACACCACCCCTCTGATCACCAT  
 CCAGCTGGAGGCCCTCTGACACGAGCCCTGTACTACCTGCTCAGCCTCTCTCCCTGTGG  
 ACATGCTGCTCTGCTCCTCACCGTCACTCCCAAGGCTCTGGCCATCTCTGGTTTGACCTCAGG  
 15 TCGATCAGCTTCCAGGCTGCTTCTCTCAGATGTTTCATCATGAACAGTTTCTTGACCATGGA  
 GTCCTGCACGTTTATGTCATGGCCATGACCGTTATGTGGCCATCTGCCATCCATTGAGA  
 TACCGTCTATCATCACTGACCAAGTTTGTGGCTAGGGCCGTGGTCTTTGTTATAGCCCGGA  
 ATGCCCTTGTCTCTCTCTGTTCCCATGCTTCTGCCAGGCTCAGATAGCTGTCAGGAAAC  
 ATAATCAAGAAGCTGACTGTCAGTAACCTGTCTGTGCCAACTCTTGTGATGACATCA  
 20 CTTTCAATCAGCTCTACCAAGTTTGTGGCAGGCTGGACTCTGTTGGGCTCTGATCTTATCCTT  
 ATTGTTATCTCTATTCTTTATATGTAAGAGTTGTGCTTAGGATCAAGGCCGAGGGTGTGCT  
 GGCCAGGCGCTTGAGCAGTGTGGTTCCCACTTCATCCTCATCCTCTCTCTCAGCAGCTCC  
 TGTGTTCTGTGTCATCACTAACCTGGCCAGGAAGAGAAATCTCCAGATGTCCCATCTCT  
 25 GCTCAACATCTGTCACCACTCATTCCCAAGCTCTGAACCCCATGTTTATGTTGTGAGA  
 ACCAAGGAGATCAAGCAGGGAATCCAAACCTGTGTAAGAGGTTGTAA (SEQ ID NO: 88)

**AOLFR47 sequences:**

MSASNITLTHPTAFLVGPGLLEHLHIWISIPFLCAYTLALLGNCTLLLIQADAALHEPMYLFLA  
 MLAAIDLVLSSSALPKMLAIFWFRDREINFFACLAQMFHLHSFSIMESAVILLAMAFDRYVAICK  
 30 PLHYTKVLGSLTIKGMMAAARAVVLTMLPLFLKCFHYKRGPIVIAHCYCEHMAVVRVLCAGD  
 TSNFNNYGIAMFIVVLDLVLVLSYIFILQAVLLLASQEARYKAFGTCVSHIGAILAFYTTVVIS  
 SVMHRVARHAAPHVHILLANFYLLFPPMNVNPIYGVKTKQIRESLGVFPRKDM (SEQ ID NO:

30

89)  
 ATGTCAGCCTCCAATATCACCTTAACACATCCAACCTGCCTTCTGTTGGTGGGGATTCCAG  
 GCCTGGAAACACCTGCACATCTGGATCTCCATCCCTTCTGCTTAGCATATACACTGGCCCTG  
 35 CTGGAAACCTGACTCTCCTTCTCATCATCAGGCTGATGAGCCCTCCGTAACCACTGT  
 ACCCTCTTCTGGGCATGTTGGCAGCCATCGAAGCTGGTCTTCTCTCTCAGCAGTCCCAAA  
 ATGCTTGCCATATTCTGGTTCAAGGATCGGAGATAAACTCTTTGGCTGTCTGGCCAGA  
 40 TGTCTCTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGTGCTGGCCATGAGCCTTTGAC  
 CGCTATGTTGGCATCTGCAAGGCACTGCCTACACCAAGGCTCTGACTGGGTCTCCCTCAT  
 CCAAGATGTGAGGCTGGCTGTGGCCGGGCTGTGACACTAATGACTCACTCCTCATCT  
 GCTGAGATGTTTCACTACTGCCGAGGCCAGTGATCGCTCACTGCTACTGTGAACACATG  
 45 GCTGTGTGAGGCTGGCGGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGTG  
 CCAGTGTATTATGTGGTGTGGACCTGCTCCTTGTATCTCTGCTTATATCTTATCTTCTGAC  
 CGACTTCTACTGCTTGCCTCTCAGAGGCCCGCTACAAGGCATTGGGACATGCTCTCTC  
 ATATAGGTGCCATCTTAGCCTTCTACACAACCTGTGGTCACTCTTCACTGATGACCGGTGA  
 50 CCGCGCATGCTGCCCTCATGTCCACATCTCTCTGCAATTTCTATCTGCTCTTCCACCC  
 CATGGTCAATCCCATATCTATGTTGTCAAGACCAAGCAATCCGTGAGAGCATCTTGGGA  
 GTATTCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

50

**AOLFR48 sequences:**

MMVDPNGNESSATYFILGLPGLLEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL  
 MMSGLDILISTSSMPKMLAIFWFSNTTIQFDACLQMAIHLSGMESTVLLAMAFDRYVAICH  
 55 PLRHAATVLTLPRTVKIGVAAVVRGAALMAPLVFVKQLPFCRSNLI.SHSYCLHQDVMKLAACDDI  
 RVNVVYGLVIVISAIGLDSLLISFSYLLIKTVLGLTREAAQAKAFGTCVSHVCAVFIFYVPFGLSM

VHRFSKRSDSPLPVILANIYLLVPPVLNPIVYGVKTEIRQIRLRLFHVATHASEP (SEQ ID NO: 91)

5 ATGATGGTGGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCCTC  
CTGGTTATGAAGAGAGGCTCAGTCTTGGTIGGCCTTCCCAATTGGTGCTCCCTCTACCTTATTGCT  
GTGCTAGGTAACCTTGACAACTCATCTCAATTGTGGCGACTGAGCACAGCCTGCATGAGCCCA  
TGTATATATTCTTTCGATGCTTTCAGGCATGTGACATCCTCATCTCCACCTCATCCATGCC  
AAAATGCTGGCCACTTCTGGTTCAATTCCACTACCATCCAGTTTGTATGCTTGTCTGTACAA  
10 GATGTTTGGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGTGCTGGCCATGGGCTTTT  
GACCGCTATGTGGCATCTGTCAACCACCTGGCCATGCCACAGTACTTACGTTGCTCGTG  
TCACCAAAATTTGGTGTGGCTGTGTGGTGGGGGGGCTGCACGTGATGGCACCCCTTCCTGT  
CTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCCTACTGCCTACACC  
AAGATGTCATGAAGCTGGCCTGTGATGATATCCGGTCAATGTCGCTATGGCCTTATCTGT  
15 CATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGCTTATTCTTA  
AGACTGTGTTGGGCTTGACACGTGAAGCCCAAGGCCAATTGGCACTTGGCTCTCTCA  
TGTGTGTGCTGTGTTCATATTCTATGTACCTTTCAATTGGATTGTCCATGGTGCATCGCTTTA  
GCAAGCGCGGTGACTCTCCGCTGCCGCTCATCTTGGCCAATATCTATCTGCTGGTTCTCTCT  
GTGCTCAACCCAATTGTCTATGGAAGTGAAGACAAAGGAGATTGCGACAGCGCATCCTTCGA  
CTTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

**AOLFR49 sequences:**

MLTFHNVCVSPSSFWLGTIPGLESJHVWLSIPFGSMYLVAVVGNVTILAVVKIERSLHQPMYFF  
LCMLAAIDLVLSTIPKLLGIFWFGACDGLDACLQMFILHCFATVESGIFLAMAFLRYAIC  
NPLRHSMLVITYTVVGRGLVSLRGLVYIGPLPLMIRLRLPLYTHVISHYSCEHMAVLAIVC  
25 DSRVNNVYGLSIGFLVLLDSVAIAASYVMIFRAVMGLATPEARLKLGTSCASHAILIFYVP  
IAVSSLIHFRQGVPPPVHTLLANFYLLIPILNPIVYAVRTKQIRESLQIPRIEMKIR (SEQ ID  
NO: 93)

30 ATGCTCACTTTTTCATAATGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCCAGG  
GCTGGAGTCCCTACACGCTTGGCTTCCATCCCTTTGGCTCCATGTACCTGGTGGCTGTG  
GTGGGGAATGTGACCATCTGGCTGTGGTAAGATAGAAGCAGCCTGACACAGCCCATG  
TACTTTTCTTGTGCATGTTGGCTGCCATTGACCTGGTTCTGTCTACTTCCACTATACCCAA  
ACTTCTGGGAATCTCTGGTTCGGTGCTGTGACATTTGGCCTGGACGCTCTTGGGCCAA  
10 TGTTCTCTTATCCACTGCTTTGCCACTGTTGAGTCAGGCATCTTCTTGCATGGCTTTTGA  
ATGCTACGTGGCCATCTGCAACCCACTACGTCATAGCATGGTGCTCACTTATACAGTGGTG  
GGTCTGTTTGGGGCTTGTCTCTCTCCCGGGGTGTTCTCTACATTGGACCTCTGCCTCTGAT  
GATCCGCTGCGGGCTGCCCTTTATAAAACCCATGTTATCTCCCACTCTATCTGTGAGCAC  
35 ATGGCTGTAGTTGCTTGACATGTGGCGACAGAGGGTCAATAATGTCTATGGGCTGAGC  
ATCGCTTCTTGGTGTGTGATCCTGGACTCAGTGGCTATTGCTGCATCCTATGTGATGATTTT  
CAGGGCGGTGATGGGGTTAGCCACTCCTGAGGCTAGGCTTAAACCTCGGGGACATCGCG  
TTCACCTCTGTGCCATCTGATCTTTATGTGCCAATTGCTGTTTCTCCCTGATTCACCG  
40 ATTTGGTCAGTGTGCTCTCTCCAGTCCACACTCTGCTGGCCAACTTCTATCTCTCATCT  
CTCCAATCCTCAATCCCAATTGTCTATGCTGTTCGCACCAAGCAGATCCGAGAGAGCCTTCT  
CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

**AOLFR50 sequences:**

MNLDFFSFLKLSLIMALNSSSWRLPQPSFFLVGIPGLEESQHWIALPLGILYLLALVGNVTILFII  
WMDPSLHQSMYFLSMLAAIDLVVASSTAPKALAVLLVRAQEIGTVCLIQMFFTTHAFSSMES  
GVLVAMALDRYVAICHLPHHSSTILHPGVIGHGMVVLVRGLLLIPFLILRLKLFQATIGHHAY  
50 CEHMAVVKLACSETTVNRAYGLTVALLVVDLVAIGVSYAHILQAVLKVPNGNEARLKHFST  
CGSHVCVILVFYIPGMFSFLTHRFGEHHVPHHVHVLAILYRLVPPALNPLVYRVKLTQKIHQ  
(SEQ ID NO: 95)

55 ATGAATTGGGATCTTTTCTCTTCTCCTCCTCAAGTCATTGATAATGGCACTTAGCAATTC  
CAGCTGGAGGCTACCCAGCCTCTCTTTTCTCGGTAGCAATTCGGGTTAGAGGAAAGC  
CAGCATGGATCGCATGCCCTCGGGCATCCTTACTCCTTGCTCTAGTGGGCAATTGTA



CCATTCTCTTCATCATCTGGATGGACCCATCCTTGCACCAATCTATGTACCTCTTCCTGTCC  
ATCGTAGCTGCCATCGACCTGGTGTGGGCTCCTCCTACTGCACCAAGCCCTTGCAGTGC  
TCTGGTTCGTGCCCCAAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTCTTACCCCAT  
GCAATCTCTCCTCCATGGAGTCAGGGGTACTTGTGGCCATGGCTCTGGATCGCTATGTAGCCA  
5 TTTGTGACCCCTTGCACCAATCCACAACTCTGCATCCAGGGGTCTAAGGGCACATCGGAAT  
GGTGGTGTCTGGTGGGGGATTACTACTCCTCATCCCTTCTCTCATCTGTTCGGAAGAACTT  
ATCTTCTGCGCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTGTGTGAAAC  
10 TTGGCTGCTCAGAAACACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTTGCTGTGGT  
TGGGCTGGATGTCTCGGCCATTGGTGTTCCTATGCCACATCTCCAGGCGAGTGTGGAAG  
GTACCGAGGAATGAGGCCGACCTTAAGGCCCTTAGCACATGTGGCTCTCATGTTGTGTGCA  
TCTGTGTTCTATATATCCCGGAAATGTTCTCCTTCTCCTACTCACCCTTGTGTGTCATCATGTA  
CCCCATCACTGTCTATGTTCTTCTGGCCATACTGATCGCCTTGTGCCACTGCACATATCC  
TCTTGTCTATAGGGTGAAGACCCAGAAGATCCACCAAGTGA (SEQ ID NO: 96)

15 **AOLFR51 sequences:**

MCQQILRDCILLIHHLCINRKKVSLVMLGPAYNHMETPASFLLVGIPGLQSSHLWLAIISLAM  
YIALLGNTHIVTAIWMDSRHEPMYCLVLAADVIVMASSVVKMVSIFCSGSSISFSACFTQ  
MFFVHLATAVETGLLTMAFDRYVAICKPLHYKRILTQVMLGMSMAITIRAHIAITPLSWMVS  
HLPCGSGNVVHSHYCEHIALARLACADPVSSLSYLSIGSSLMVGSVDVAFIAASYILILKAVFGLSS  
20 KTAQLKALSTCGSHVGMALYYLPGMASIYAALWGDQVPLHTQVLLADLYVPIATLNPYH  
GMRTKQLRERIRWSYLMHVLFDHNSNLGS (SEQ ID NO: 97)

ATGTGTCAACAAATCTTACGGGATTGCATCTTCTCATACATCATTTGTGCATTAACAGGA  
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCAACAATAAGGAAACCCCTGGCTC  
25 CTCTCCTCTTGTGGGTATCCAGGACTGCAATCTTCACATCTTGGCTGGCTATCTCACTGA  
GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCTGCTGCAATCTGGATGGA  
TTCCACTCGCATGAGCCCATGTTATGCTTCTCTGTGTCTGGCTGCTGTGACATTTGTA  
TGGCCTCCTCGGTGGTACCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG  
CTTTAGTGCTGTGTTTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG  
30 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACACAGA  
GAATTTCTACGCCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT  
AGCCATAACTCCACTGAGTTGGATGGTGAGTCACTACCTTCTGTGGCTCCAATGTGGTT  
GTCCACTCTACTGTGAGCACATAGCTTTGGCCAGGTAGCATGTGCTGACCCCGTGCCCA  
GCAGTCTCTACAGTCTGATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCCTTCAATTGCT  
35 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA  
AGCATTAAGCACATGTGGCTCCATGTGGGGTTATGGCTTTGTACTATCTCACTGGGATG  
GCCTTCCATCTATGGCGCTGGTTGGGGCAGGATGTAGTGCCTTGCCACACCACTGCTCG  
TAGCTGACCTGTACGTGATCATCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC  
CAAAACAACGCGGGAGAGAAATAGGAGTTATCTGATGCATGTCTCTTTGACCATTCCAAC  
40 CTGGGTTCATGA (SEQ ID NO: 98)

**AOLFR52 sequences:**

MLGPAYNHMETPASFLLVGIPGLQSSHLWLAIISLAMYITALLGNTHIVTAIWMDSRHEPMY  
CLVLAADVIVMASSVVKMVSIFCSGSSISFSACFTQMFFVHLATAVETGLLTMAFDRYV  
45 AICKPLHYKRILTQVMLGMSMAVTRAVTFMTPLSWMNHLPCGSGNVVHSHYCKHIALAR  
LACADPVSSLSYLSIGSSLMVGSVDVAFIAASYILILRAVFDLSSKTAQLKALSTCGSHVGMALY  
YLPGMASIIYAALWGDQVPLHTQVLLADLYVPIATLNPYHGMRTKQLLEGIWSYLMHVLFDH  
SNLGS (SEQ ID NO: 99)

50 ATGCTGGGTCCAGCTTACAACCACACAATGGAACCCCTGCCTCCTTCTCCTTGTGGGTA  
TCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGAGTGCCATGTACATCAC  
AGCCCTGTAGGAAACCCCTCATCGTGACTGCAATCTGGATGGATTCACCTCGGCATGAG  
CCCATGTATTGCTTCTGTGTGTTCTGGCTGCTGTGGAATTTGTTATGGCCTCCTCCGTGGT  
ACCAAGATGTGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGTGTTGTTT  
55 ACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGACCATGG  
CTTTTGACCCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCAGCCCTCA

AGTGTAGCTGGGAATGAGTATGGCCGTACCATCAGAGCTGTCACATTCATGATCCACTG  
AGTTGGATGATGAATCATCTACCTTTCTGTTGCTCCAAATGTGGTTGTCCACTCTACTGTAA  
GCACATAGCTTTGCCCAGGTTAGCATGTGCTGACCCCGTCCAGCCAGCTCTCTACTAGTGT  
ATITGGTTCTCTCTTATAGTGGGGCTCTGATGTGGCCCTTCATTTGCTGCTCTATATCTTAA  
5 TCTCAGGGCAGATTGTGATCTCTCTCAAAGACTGCTCAGTTGAAAGCATTAAAGCACATGT  
GGCTCCCATGTGGGGGTTATGGCTTTGACTATCTACCTGGGATGGCATCCATCTATGCGG  
CCTGGTTGGGGCAGGATATAGTGCCCTTGACACCCAAAGTGTCTAGCTGACCTGTACGT  
GATCATCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAACAATTGCTGGAG  
10 GGAATATGGAGTATCTGATGCACCTTCTCTTTGACCACTCCAACCTGGGTTTCATGA (SEQ  
ID NO: 100)

#### AOLFR54 sequences:

MSDSNLSDNHLPDITFLTGIPGLEAAHFWIAIPFCAMYLVALVGNAAILVIAMDNALHAPMY  
LFLCLLSLDLALSSTVTPKMLAILWLHAGEISFGGCLAQMFCVHSIYALESSILLAMAFDRYVA  
15 ICNPLRYTTLNHAIVIGRJGFVGLFRSVAIVSPFIFLLRRLPYCGHRVMTHTTYCEHMGHARLACA  
NITVNIVYGLTVALLAMGLDSILIAISYGFILHAVFHLPSHDAQHKALSTCGSHIGILVFYIPAF  
SFLTHRFGHHEVPKHVHIFLANLYLVPPVLNIPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID  
NO: 101)

20 ATGTCAGATTCACCACTCAGTGATAACCATCTCCAGACACCTTCTTCTTAACAGGGATCC  
CAGGGCTGGAGGCTGCCACTTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTGTAGC  
ACTGGTTGGAAATGCTGCCCTACCTGGTCAITGCCATGGACAAATGCTCTTCATGCACCT  
ATGTACCTCTTCTCTGCCCTTCTCTACTACAGACCTGGCTCTCAGTTCTTACCACCTGTGCC  
25 CAAGATGCTGGCCATTTTGTGGCTCCATGCTGGTGAGATTTCCTTTGGTGGATGCTCGGCC  
CAGATGTTTGTGTGCCATTCTATCTATGCTCTGGAGTCTCGATTCTACTTGGCATGGCCCTT  
TGATAGGATATGGGCTATCTGTAACCCATTAAGGTATACAACCATTTCTCAACCATGCTGTC  
ATAGGCAGAAATGGCTTTGTGGGCTATTCCGTAGTGTGGCTATTGTCTCCCCCTTCATCTT  
CTTGCTGAGGCGACTCCCTACTGTGGTCACCGTGTCTAGACACACACATACGTGAGCAT  
ATGGGTCATCGCCGACTGGCCTGTGCCAACATCACTGTCAATATTTGCTATGGGGTAACTGT  
30 TGGCTCTGGCCATGGGACTGGATTCCATTTCTATTGCCATTCTTCACTGGCTTTTATCTCT  
CATGCAGTCTTTACCTTCCATCTCATGATGCCAGCACAAGCTCTGAGTACCTGTGGCT  
CCACATTATGATCATCTCGGTTTCTACATCCCTGCCCTTCTCTCTCTCTCCACCCGCG  
TTTGGTACCAGCAAGTCCCAAGCATGTGACCATCTTCTGGCTAATCTCTATGTGCTGG  
35 TGCCCTGTACTCAATCTATTCTATGAGCTGAACCAAGAGATTGGGAGTCGACT  
TCTAAAAGCTGTTACCTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)

#### AOLFR57 sequences:

MSFQVTYMFYLHWTMEKSNSTLFIILGFSQKNIEVLFCVFLFCYIAIWMGNLLIMISITCQ  
LIHQPMYFFNLNLSDLCYTSVTPKLMVDLLAERKTSYNNCMIQLFTTHFFGGIEFILTGM  
40 AYDRYVAICKPLHYTIIMSRQKNTIIVCCTGGFIHSASQFLITFVPFCGPNEDHYFCDDYPLL  
KLACSNHIMIGLLVIANSGLIALVTFVLLSYVFILYTIRAYSAERRSKALATCSSHVIVVVLFF  
APALFIYIRPVITFSEDKVFALFYTIAPMFNPLYTLRNTEMKNAMRKVWCQILLKRNQLF  
(SEQ ID NO: 103)

45 ATGTCATTTCAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAGCAATAATA  
GCATTTGTTTATTCTCTTGGGGTTTCCCAAATAAGAACATGAAGTCTCTGCTTGTGTA  
TTATTTTGTGTTGCTACATTGCTATTGGATGGGAACTTACTATAATGATTTCTACAC  
GTGCACCCAGCTCATTCACCAACCCATGTATTTCTCTCTCAATTACCTCTGCTCCGACC  
TTTGCTACACATCCACAGTGACCCCAAAATTAATGGTTGACTTACTGGCAGAAAGAAAGAC  
50 CATTTCTCTATAATACTGTATGATACAACTCTTACCACCCATTTTITGGAGGCATAGAGA  
TCTTCATTTCTCACAGGGATGGCCTATGACCGCTATGTGGCCATTTGCAAGCCCTGCACTA  
CACCATTATTAACAGGCAAGGCAAAAGTGAACACAATCATCATAGTTTGTGTACTGGGGGA  
TTTATACATCTGCCAGTCAGTTTCTTCTCACCATCTTTGTACCAATTTGTGGCCCAAATGA  
GATAGATCACTACTCTGTGATGTGATCTCTTGTGGAATGGCCTGTTCTAATATACAGA  
55 TGATAGGTCTCTTAGTCATTGCTAATTCAGGCTTAATTGCTTTGGTGACATTTGTGTCTTG  
TTGTTGTCCTTATGTTTTATATTGATACCATCAGAGCATACTCTGCAGAGAGAGCGCAGCA

AAGCTCTTGCCACTTGTAGTTCTCATGTAATTGTTGTGGTCTGTTTTTGCTCCTGCATTG  
 TTCATTTACATTAGACCGGGTCAACAACATTCTCAGAAGATAAAGTGTTTGCCCTTTTTTATAC  
 CATCATTCGCTCCCATGTTCAACCCCTCTCATATACCGCTGAGAAACACAGAGATGAAGAAC  
 GCGCATGAGGAAAGTGTGGTGTGTGCAAACTACTCTGAAAAGAAATCAACTTTTCTGA (SEQ  
 ID NO: 104)

**AOLFR58 sequences:**

MFMSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFISLGNMQNSQSVTFE  
 VLLGLSQPNPVQEIFVVFVLYIATVGGNMLIVVLTSSPALLVSPMYFVLGLFSLDACFSSVI  
 TPKMIVDSLVYTKTISFEGCMQMLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL  
 CGILMGVAWTGGLLHSMIQILFTQLPFCGPNVINHFMCDDLPLLELACTDTHIFGLMIVNSG  
 FICINFSLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVILFFVPCIFVYTRPPSAFSLDKMA  
 AIFYIILNPLLNPLYITFRNKEVKQAMRRRIWNRMLMVSDKENIKL (SEQ ID NO: 105)

ATGTTCTCAATGACAACAGAAGCACTCAATAATTTGCACTTGGATGTACCAACTTGTAA  
 TGACTATGATACCAACAAATTGATCTGAAGCAAAATTTCTTTGTCTCAATTGACAGACTATA  
 CATGATCCCTGTTGGAGCTTTCATCTTTTCTTGGGAAACATGCAAAACCAAGCTTTGTGA  
 ACTGAGTTGTCTCTCTGGGACITTCACAGAATCCAAATGTTACAGGAAATAGTATTTGTTG  
 TATTTTGTGTTGCTCATGTCGAACCTGTTGGGGGCAACATGCTAATTGTAGTAACTACTCTC  
 AGCAGCCCTGCTCTCTCTGGGTCTCTCATGTACTCTCTTGGGCTGCTGCTCTCTCTGGA  
 TGCCTGCTCTCTCATCTGTGTCATCACCACAAAGATGATTGTAGACTCCCTCTATGTGACAAAA  
 ACCACTCTCTTTGAAGGCTGCATGATGCACTCTTTGCTGAACACTTCTTTGCTGGGTGG  
 AGGTGATTGTCTCCACAGCCATGGCCTATGATCGTTATGTGGCCATTGTGCAAGCCCTTGCAT  
 TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG  
 GGCCTCTTGCATTCATGATACAAATCTTTTACTTTCCAGCTTCCTTTTGTGGCCCAA  
 TGTCTACATCACTTTATGTGTGACTGTACCCGTTACTGGAAGCTTGCCTGCACTGATAC  
 ACATCTTGGCCTCATGGTGGTCAACAAGTGGGTTTATCTGCATCAATAACCTTCTCTTC  
 TTGCTTGTCTCCTATGCTGTCTCTTGTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG  
 GAAAGCGCTCTCCACCTGTGATCTCACATTGCTGTGTGATTTTGTTCTTTGTCCCATGCA  
 TATTTGATATACAGCACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTAT  
 ATCATCTTAAATCCCTTGTCTCAATCTTTGATTTACACTTTTCAGGAATAAGGAAGTAAAC  
 AGGCCATGAGGAGAAATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA  
 AACTTAA (SEQ ID NO: 106)

**AOLFR59 sequences:**

MGDWNNSDAVEPILRGFGLEYVHWSLSILFCLAYLVAFMGNVTLSVIWIESSLHQPMYYFI  
 SILAVNDLMSVIGTITMLAVLWDLDAPEIQASACYAQLFFHITFTLESSVLLAMAFDRFVAICH  
 PHYPYLTNSVSLGKGLACLRLSGVLPPLLRHYHYCHGNALSHAFCLHQDVLRLSCIDA  
 RTNSIYGLCVVIATLGVDSIFILSYVLLILNTVLDIASREEQLKALNTCVSHICVVLFFVPIVIGVS  
 MVHRFGKHLSPVHILMADIYLLPPVLPVIVSVRTKQIRILGILHKFVLRRLF (SEQ ID NO:  
 107)

ATGGGAGACTGGAAATAACAGTGATGCTGTGGAGCCCATATTTATCTCGAGGGGTTTTCTGT  
 GACTGGAGATATGTTCACTTCTGGCTCTCCATCCTCTCTGTCTTGCAATATTTGGTAGCATTT  
 ATGGGTAAATGTTACCATCTGCTGTGTCATTGGATAGAATCCTCTCTCCATCAGCCCATGTA  
 TTACTTTATTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCCTGTCTACACTTCCCACCA  
 TGCCTTGTGTTGTTATGGTGTGGATGCTCCAGAGATCCAGGCAAGTGTGCTATGTCAGCT  
 GTTCTTCATCCACACATTCACATCTCTGGAGTCTCAGTGTGTCTGGCCATGGCCCTTGACC  
 GTTTTGTGTCATTTGCTGCAATCCATGCACTACCCACCATCTCCACCAAGTGTAAATGGC  
 AAAATTTGGTTTGGCTGTTTGTGTCAGGAAGCTTGGGAGTTGTACTTCCACACTCTTGTACT  
 GAGACACTATCACTATGCCATGGCAATGCCCTCTCTACGCCTTCTGTTTGGACAGGAT  
 GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTTATGGGCTTTGTGTAGTCA  
 TTGGCACTAGGTTGGATTCAATCTTCATACTTCTTCTATGTTCTGATTTCTTAATACT  
 GTGCTGGATATTTGCATCTGTTGAAGAGCAGCTAAAGGCACCTCAACATGTTGATCCCAT  
 TCTGTGTGGTGCTTATCTCTTTGTGCCAGTTATTTGGGGTGTCAATGGTCCATCGCTTTGGG  
 AAGCATCTGTCTCCCATAGTCCACATCTCATGGCAGACATCTACCTTCTTCTCCCCCAGT

CCTTAACCCATTATTGTCTATAGTGTGAGAACAAAGCAGATTTCGTCTAGGAATTCTCCACAAG  
TTTGTCTTAAGGAGGAGGTTTAA (SEQ ID NO: 108)

**AOLFR60 sequences:**

5 MFLPNDTQFHPSSFLLLGIPGLETLHIWIGFPFCVYMIALIGNFTILLVIKTDSSHLQPMFYFLA  
MLATTDVGLSTATIPKMLGIFWINLRIIEEACLTQMFHNFNTLMESAVLVAMAYDSVAICN  
PLQYSAILTNKVSVSIVGLGVFVRALIFVIPSILILRLPFCGNHVIPHTYCEHMGHLASCSIKINI  
IYGLCAICNLVFDITVIALSYVHILCAVRLPTEHRLKSLSTCGSHVVCVILAFYTPALFSFMTHC  
FGRNVPRYIHHILLANLYVVVPPMLNPVIYGVRTKQYKCVKILLQEQGMEKEEYLIHTRF  
10 (SEQ ID NO: 109)

ATGTTCTCTCCCAATGACACCCAGTTTACCCCTCCTCCTTCTGTGTGCTGGGGATCCCAGG  
ACTAGAAACACTTCACATCTGGATCGGCTTTCCCTTCTGTGCTGTGTACATGATCGCACTC  
15 ATAGGGAACCTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCCTACACAGCCCATGT  
TCTACTTCTCGGCCATGTTGGCCACCAGCTGATGTGGGTCTCTCAACAGCTACCATCCCTAA  
GAGTCTTGGAAATCTCTGGATCAACCTCAGAGGGATCATCTTTGAAGCTCGCCTCACCAG  
ATGTTTTTATCCACAACCTTCACTTATGGAGTCAGCAGTCTTGTGGCAATGGCCTATG  
ACAGATGTGGCCATCTGCAATCCACTCCAATATAGCGCCATCCCTACCAACAAGGTGTG  
20 TTCTGTGATGTGGTCTTGGTGTGTTGTGAGGGCTTTAATTTTCGTCATTCCCTCTATCTC  
TTATATTGCGGTGCGCCTTCTGTGGGAATCATGTAATTCGCCACACCTATGTGAGCAAT  
GGGCTTGCTCATCTATCTGTGCGCAGCATCAAAATCAATATTATTTATGGTTTATGTGCCA  
TTTGAATCTGTGTTGTGACATCAGCTCATTGCCCTCTCTTATGTGCATATTCTTTGTGCT  
GTTTTCGCTTCTCTCATGATGAGCCCGACTCAAGCTCCCTCAGCAGCATGTGGTTCACATGT  
25 GTGTGTAATCCTTGCCTTCTATACACAGCCCTCTTTCTCTTATGACTCATTGCTTTGGCC  
GAAATGTGCCCGCATATATCCATATACTCTAGCCCAATCTCTATGTGTGGTGCCCAACAA  
GCTCAATCCTGTATATATGGAGTCAGAACCAAGCAGATCTATAAATGTGTAAAGAAAAT  
ATTATTGACAGGAACAAGGAATGGAAAAGGAAGTACCTAATACATACGAGGTTCTGA  
(SEQ ID NO: 110)

**AOLFR61 sequences:**

MSIINTSVVEITTFVLVGMGPLEYAHIWISIPICSMYLIAILNGNTILFIHKTEPSLHGPMMYFSLML  
AMSDLGLSLSSLPVTLISLFLNAPETSSSACFAQEFFHGFVSLESSLIMSFDRFLAHNPLRYT  
SILTTVRVAQIGIVFSFKSMMLVLPFPFTLRLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVY  
35 GFGALCLMVDIFILIAVSYTLILKTPVGLASKKEELKALNTCVSHICAVIIFLPIINLAVVHRFAG  
HVSPLINVLNMANVLLVPLMKPIVYCVKTKQIRVRVVAKLQWKI (SEQ ID NO: 111)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTGTTGGGATGCCAG  
GGCTAGAATATGCACACATCTGGAATCTCTATCCCATCTGCAGCATGTATCTTATTTGCTATT  
CTAGGAAATGGCACCATTCTTTTATCATCAAGACAGAGCCCTCCTTGCATGGGCCCATGT  
40 ACTATTTTCTTCCATGTGGCTATGTCAGACTTGGGTTTGTCTTATCATCTCGCCACT  
GTGTAAAGCATCTTCCGTGTTCAATGCCCTGAAACTTCTCTAGTGCCCTGCTTGGCCAGGA  
ATTCTTCATTATCGGATTCTCAGTACTGGAAGTCTCAGTCTCTGATCATGTTCATTGATA  
GATTCCTAGCCATCCACAATCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC  
45 CCAAAATAGGGATAGTATTCTCTTAAAGAGCATGCTCCTGGTCTCTCCCTTCCCTTCACT  
TAAGAAGCTTGAGATATTGCAAGAAAAACCAATTATCCCATCTCACTGTCTCCACAGGA  
TGTCATGAAGTTGGCCTGTTCTGACAAACAGAATTGATGTTATCTATGGCTTTTGTGGAGCA  
CTCTGCCCTTATGGTAGACTTTATTTCTCATGTGCTGTCTACACCTGATCCTCAAGACTGT  
ACCGGGAATTTGATCCACAAAAGGAGGAGCTTAAAGCTTCAATACTTGTGTTTACACATC  
TGTGCAGTGTACATCTTCTACTGCCCATCATCAACCTGGCCGTTGTCCACCCGTTTGGCCG  
50 GCATGTCTCTCCCTCAATTAATGTTCTCATGGCAAAATGTTCTCTCACTGTGACTCCGCTGA  
TGAAACCAATTGTTTATTGTGTAATAAATAACAGATTAGAGTGAGAGTTGTAGCAAAAT  
GTGTCATGGAAGATTAA (SEQ ID NO: 112)

**AOLFR62 sequences:**

55 MFYHNKSIHFVTFFLIGIPLEDHFMWISGPFCSVYLVALLGNATILLVIKVEQTLREPMFYFL  
AILSTIDLALSATSVPRLMGIFWFDAAHEINYGACVAQMFLIHAFTGMEAIEVLLAMAFDRVVAIC

APLPHYATILTSLVLVIGSMCIVIRPVLLTLPVMVLIYRLPFCQAHIIAHSYCEHMGIAKLSCGNIRI  
NGIYGLFVVSFFVLNLVLIGISYVYLRAVFRLPSPHDAQLKALSTCGAHVGVICVFPYPSVFSFLT  
HRFGHQIPGYIHILVANLYLIIPPSLNPHYGVRTKQIRERVLYVFTKK (SEQ ID NO: 113)

- 5 ATGTTTATCAACAAGAGCATATTTCAACCCAGTCACATTTTCTCTATTGGAATCCCGAGG  
TCTGGAAGACTTCCACATGTGGATCTCCGGGCCCTTCTGCTCTGTTTACCTTGTGGCTTTCG  
TGGGCAATGCCACCATCTGCTAGTCATCAAGGTAGAACAGACTCTCCGGGAGCCCATGTT  
CTACTTCTGGGCCATCTTTCCACTATTGATTGGCCCTTCTGCAACCTCTGTGGCTCGCA  
10 TGCTGGGTATCTTCTGGTTTGTAGTCTCAGGAGATTAACTAGGAGCTTGTGTGGCCAGAT  
GTTTCTGATCCATGCTTCTCACTGGCATGGAGGCTGAGGCTCTACTGGCTATGGCTTTTGAC  
CGTTATGTGGCCATCTGTGTCCACTACATTACGCAACCATCTTGACATCCCTAGTGTGGT  
GGGCATTAGCATGTGCATTGTAATTGTCGCCGTTTACTTACATCTCCCATGGTCTATCTTA  
TCTACCGCTACCCCTTTGTGACGGCTCACATAATAGCCCATTCCTACTGTGAGCACATGGG  
15 CATTGCAAAATGTCTGTGGAAACATTCGTATCAATGGTATCTATGGGCTTTTGTAGTTT  
CTTTCTTTGTCTGAACCTGGTGCTCATTGGCATCTCGTATGTTTACATTCTCCGCTGCTGC  
TTCCGCTCCCATCACATGATGCTCAGTAAAAGCCCTAAGCACTGTGGCGCTCATGTG  
GAGTCATCTGTGTTTCTATATCCCTCAGTCTTCTTCTTCTACTCATCGATTGGACAC  
CAAAATACAGGTTACATTCACATCTTGTGTGCCAATCTCTATTTGATTATCCCAACCTCTCT  
20 CAACCCCATCATTTATGGGGTGAGGACCAACAGATTCGAGAGCGAGTGCTCTATGTTTT  
ACTAAACAAATAA (SEQ ID NO: 114)

#### AOLFR63 sequences:

- MSIINTSYVEITFFVLVGMPLGLEYAHIWISIPICSMYLIALLNGNTILFIKTEPSLHEPMYYFLSML  
AMSDLGLSSSLPTVLSIFLNAPEISSNACFAQEFFHGHFSVLESSVLFDRFLAIHNPRIYTS  
25 ILTIVRVYQIGIVSFKSMILLVLPFPFLRLNRLYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY  
GFFGALCLMVDFILIAVSYTLILKTVLGIASKKEQLKALNTCVSHICAVIIFYLPIINLAVVHRFAR  
HVSPLINVLMAVLLVLPPLTNPIVYCVKTKQIRVRVVAKLQQRKI (SEQ ID NO: 115)

- 30 ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTGGTTGGGATGCCAG  
GGCTAGAAATGACACACATCTGGATCTCTATCCCATCTGCAGCATGTATCTTATGCTATT  
CTAGGAAATGGCAACCATCTTTTATCATCAAGACAGAGCCCTCCTGTCATGAGCCCATGT  
ACTATTCTTCTTCAATGTTGGCATGTGTCAGACTTGGGTCTGCTTTATCATCTCTGCCCACT  
GTGTTAAGCATCTCCTGTTCAATGCTCCTGAAATTCATCCAATGCCCTGCTTGTGCCAGGA  
35 ATTCTTCATTATGAGTTCTCAGTACTGGAGTCTCAGTCCCTCCTGATCATGTCAATTGATA  
GATTCTAGCATCCCAACCCCTCGAGATACACCTCAATCCTGACAACCTGTCAGAGATTGC  
CCAAATAGGGATAGTATTCTCCTTAAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACCT  
TAAGAAACTGTGAGATATTGCAAGAAAAACCAATTATCCCATCTCTACTGTCTCCACAGGA  
TGTCATGAAGTTGGGCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTGTGGAGCA  
40 CTCTGCCATTATGGTAGACTTTATCTCATGTCTGTGCTTACACCTGATCCTCAAGACTGT  
ACTGGGAATTGCATCAAAAAAGGAGCAGCTTAAGGCTCTCAATCTGTGTTTGCACACATC  
TGTGCACTGATCATCTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGGCCCG  
GCATGTCTCTCCCTCATTAATGTTCTCATGGCAATGTTCTCCTACTGTGACCTCCACTGA  
CGAACCCAAATGTTTATGTGTAAAACTAAACAGATTAGAGTGAGAGTGTGAGCAAAAT  
50 GTGTCAACGGAAGATTAA (SEQ ID NO: 116)

#### AOLFR64 sequences:

- MTILLNSSLQRATFELTFGQGLEGLHGWISIPFCFIYLTVLGNLTLHVICTDATLHGPMPYYFLG  
MLAVIDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFHITLSSMESSVLLSMSIDRSVAVCNPL  
HDSTVLPACIVKMGSSSVLRSALLILPLPFLKRFQYCHSHVLAHAYCLHLEIMKLACSSIIYN  
50 HIYGLFVVACTVGDSLTLILFISYAILRLTVLSIAHQERLRLNCTVSHICAVLLFYIPMIGLSLV  
HRFGHEHLPRVVHLMFMSYVYLLVPPLMNPYISIKTKQIRQRIHKFQFIKSLRCFWKD (SEQ ID  
NO: 117)

- 55 ATGACAATTCTTCTTAATAGCAGCCTCCAAAGAGCCACTTTCTCTGACGGGCTTCCAA  
GTCTAGAAAGCTCCATGGCTGGATCTCTATCCCTTCTGCTCATCATCTGACAGTATCT  
TTGGGAAGCACTCACCATTCTCCACGTCATTGTTACTGATGCCACTCTCCATGGACCATGTT

ACTATTTCTTGGGCATGCTAGCTGTACAGACTTAGGCCTTTGCCTTTCCACACTGCCACT  
GTGCTGGGCATTTTCTGGTTTGATACCAGAGAGATTGGCATCCCTGCCTGTTTCACTCAGC  
TCTCTTCTATCCACACCTTGTCTTCAATGGAGTTCATCAGTTCTGTATCCATGTCCATTGAC  
CGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCACCGTCTGCACCTGCATGTATGT  
5 CCAAGTAGGGGCTAAGCTCAGTGCTTAGAAGTCTCTCCTCATCCTCCCTCCCTGATCTTCTC  
CTGAAGCGCTTCCAATCTGCCACTTCCATGTGCTGGCTCATGCTTATTTGTCTTCACTCCGGA  
GATCATGAAGCTGGGCTGCTTAGCATCAITTTGCAATCAGATCTATGGGCTTGTGTTGTG  
GCTGCACCGTGGGTGTGGACTCCCTGCTCATCTTTCTCTCATACGCCCTCATCTTTCGCAC  
10 CTGTGCTCAGCATTGCTCCACCAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCAT  
ATCTGTGCTGTACTGTCTCTTACATCCCAATGATTGGCTTGTCTCTGTGCATCGCTTTGG  
TGAAACATGTGCCCCGCGTTGTACACCTCTCATGTCTATGTGTATCTGCTGGTACCACCC  
TTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAATTCCGACGCGCATGTTTGAAGAA  
GTTTCAGTTTATAAAGTCACTTAGGTGTTTTTGAAGGATTAA (SEQ ID NO: 118)

# **AOLFR65 sequences:**

MAGRMTSNHTQFHPSFLLLGIPLEDVHIWIGVFFVYVLLGNTALLFVIQTEQSLHEPM  
YIFLAMLDLSTLSTIPKMLGIFWNTKEISFGGCLSHMFFHHFTAMESIVLVAMAFDRYI  
AICKPLRYTMLTTSKIISLAGIAVLRSLYMVVPLVFLRLPFCGHRIIPYCEHMGIRLACAS  
15 IKVNIIRFLGNISLLLDVILJLSYVRILYA VFLPSWEARLKALNTCGSHIGVILAFFTPAFFSFL  
THRFGNINPQYHIILANLYVVVPPALNPVYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCATCTCTTCTTCACTGCT  
GGGTATCCGAGGCTAGAAGAATGTGCACATTGGATTGGAGTCCCTTTTCTTTGTGTAT  
CTTGTTGGCACTCGTGGGAAACACTGCTCTCTGTGTTGTGATCCAGACTGAGCAGAGTCTCC  
25 ATGAGCTATGTACTACTTCTCGGCCATGTGGATTCCATTGACCTGGGCTGTCTACAG  
CACCATCCCAAAATGTGGGCCATCTCTGGTTCATACCAAAGAAATATCTTTGGAGGC  
TGCCCTTCTCATGTGTTCTTCTATCCATTTCTCATGCTATGGAGAGCATGTGTTGGGCG  
CATGGCCCTTGACCGCTACATTTGCCATTGCAAACCTCTTCGGTACACCATGATCCTCACCA  
30 GCAAAATCATCAGCCTATTGCAGGCATGTGCTGCTGAGGAGCCTGTACATGGTTGTTC  
ACTGTGTTTCTCTCTCTGAGGCTGCCCTTCTGTGGGCATCGTATCATCCCTCATACTTAT  
GTGAGCAGATGGGCATGCCCCTGTGGCCTGTGCCAGCATCAAAGTCAACATTAGGTTTGG  
CCTTGGCAACATATCTCTCTGTACTGGATGTATCTCTTATTTCTCTCTATGTACAGGA  
TCTGTATGCTGCTCTCTGCTGCCCTCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGT  
35 GGTCTCATGCTGTATCTTAGCTCTTTTACACAGCATTTTTCATTCTTGACACA  
TCGTTTGGCCATAATATCCACAGTATATACATATTATATTAGCAACCTGTATGTGGTGT  
TCCCACAGCCCTCAATCCTGTATCTATGGAGTCAGGACAAAGCAGATTCGAGAGAGAG  
TGCTGAGGATTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)

# **AOLFR66 sequences:**

MSFLNGTSLTPASFILGIPLEDVHLWISFPLCTMYSIATGNFLMYLIYDEALHRPMYVFL  
ALLSFTDVLMTSTLPTNLFILWNLKEIDFKACLAQMFFVHTFTGMESGVLMMLDHCVAI  
40 CPLRYATILTNSVIKAGFLTFLRGVMLVIPSTFLTKRLPYCKGNVPIHTYCDHMSVAKISGN  
VRVNAIFYGLVALLJGGFDILCTITSYTMILQAVVSLSSADARQKAFSTCTAHFCAIYLTVVPAFF  
TFFTHHFGGHTIPLHHIIMANLYLLMPPTMNPVYGVKTRQVRESVIRFLKGKDNHSNF (SEQ  
45 ID NO: 121)

ATGTCAATTCTAAATGGCACCAGCCTAACTCCAGTTCATTATCTCTAAATGGCATCCCTG  
GTTTGAAGATGTGCATTTGGGATCTCCTTCCCACTGTGTACCATGTACAGCATTCGTATT  
ACAGGGAACCTCGGCCCTTATGTACCTCATCTACTGTGATGAGGCCCTTACACAGACCATGT  
50 ATGTCTCTCTTGGCCCTCTTCTCTCACAGATGTGCTCATGTCAGCAGCACACCTTCCCAAC  
ACTCTTTCATATTGTGGTTAAATCTCAAGGAGATTGATTTTAAAGCCTGCTCGCCAGAT  
GTTCTTTGTGCAACCTTACAGGGATGGAGTCTGGGGTGTCTATGCTCATAGGCCCTGGAG  
CACTGTGTGGCCATCTGCTTCCCTCTGCGTTATGCCACCATCTCACTAAATTCAGTATTGTC  
TAAAGCTGGGTTCTCACTTTTCTTGGGGTGTGATGCTGTATCCCTTCCATCTTCTCTCA  
55 CCAAGCGCCTTCCATATGCAAGGGCAACGTATACCCACACCTACTGTGACCACATGTC  
TGTGGCCAAGATATCTTGTGGTAATGTACAGGTTAAAGCCATCTATGGTTTGATAGTTGCC



# **AOLFR69 sequences:**

MSYSIYKSTVNIPLSHVSVHSFCHNMNCNFMHIFKVLDFNMKNVTEVTLFVLKGFTDNLELQ  
 TIEFFFLFLAYLFTLMGNLGLILVVRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTTKN  
 5 KVISFLGCVAVQLFACSGFTTECFLLAAMAYDRYVAIYNPLLYSVMSPRVYMLINXSVAGI  
 LHATHIVTATFSLSCFGANEIRRVFCDIPPLLAISYSDTHTNQLLLFYFVGSIELVTILIVLISYGLIL  
 LAILKMYSAEGRKRVPSTCGAHLTGVSIIYGTILFMYVRPSSSYASDHMDMIVSIFYTIVIPLLNPV  
 IYSLRNKDVKDSMKKMFNGKQVINKVYFHTKK (SEQ ID NO: 127)

10 ATGTCGTACAGTATATACAAGACACAGTTAACATCCCCCTTGAGTCATGGTGTGTGTTCAATT  
 CTTTTTGTGCATAAATGAAGCTGTAACCTTTATGCATATCTTCAAGTTTGTGTTCAAGTTCAAC  
 ATGAAGAATGTCAGTGAAGTTACCTTATTTGTAAGTGAAGGGCTTACAGACAACTCTGAAAC  
 TGCAGACTATCTCTCTCTCTCTCTGTTTCTAGCAATCTACCTCTTCACTCTCATGGGAAATTA  
 GGACTGATTTAGTGGTCATTAGGGATTCCACAGCTCCACAAACCCATGTACTATTTCTGTA  
 15 GTATGTGTTCTCTGTTGGATGGCTGCTATTCTCAGTTATTAACCCAAATATGTTAGTAGAT  
 TTTACGACAAAGATAAAGTCACTTTCATTCTCTGGATGTGTAGCACAGGTGTTTCTTGCTT  
 GTAGTTTGTGGAAACACAGAATGCTTCTCTTGCTGCAATGGCTTATGATCGCTATGTAGC  
 TCTACACACCTCTCTCTGTAATTCAGTGAGCATGTACCCAGAGCTACATGCCCACCTCATC  
 AATGCTTCTATGTTGCTGGCATTTTACATGCTACTATACATACAGTGGCTACATTTAGGCT  
 20 ATCCCTCTGTGGAGCCAATGAAATTAGGCGTGTCTTTGTGATATCCCTCTCTCTCTGTCTA  
 TTTCTTATCTGACAGCTACACAAACACAGCTTCTACTCTTCTACTTTGTGGGCTCTATCGAG  
 CGGTGCTACTATCCTGATTGTTCTGATCTCTATGGTTTGATTCTGTTGGCCATCTGAAGAT  
 GTATTCTGCTGAAGGGAGGAGAAAAGTCTTCTCCACATGTGGAGCTCACCTAACTGGAGT  
 GTCAATTTATATGGGACAACTCCTCTCATGTATGTGAGACCAAGTCCAGCTATGCTCG  
 25 GACCATGACATGATAGTGTCAATATTTACACCAATGTATCCCTTGCTGAATCCCGTCTCAT  
 CTACAGTTTGAGGAAACAAAGATGTAAAAGACTCAATGAAAAAATGTTTGGGAAAAATCA  
 GGTTATCAATAAAGTATATTTTCATACTAAAAATAA (SEQ ID NO: 128)

# **AOLFR70 sequences:**

MDSTFTGYNLYNLQVKTEMDKLSSGLDIYRNPLKNKTEVTMFLTGTFDDFELQVFLFLFFAI  
 YLFTLIGNLGLVVLVIEDSWLHNPMMYYFLSVLSFLDACYSTVVTPKMLVNFLLAKNKSISFIGCA  
 TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVMSPRVYPLITASYVAGILHATHIVA  
 30 TFSLSFGCSNIRHVFCMDPPLLAISCSDTHTNQLLLFYFVGSIEIVTILIVLISCDFILLSILKMHS  
 KGRQKAFSTCGSHLTGVTTYHGTILVSYMRPSSSYASDHDIIVSIFYTIVIPKLNPHIYSLRNKEVK  
 KAVKKMLKL VYK (SEQ ID NO: 129)

35 ATGGACTCCACTTTACAGGGCTATAACCTTTATAACCTGCAAGTAAAACTGAAATGGACA  
 AGTGTGTCATCAGGTTTGGATATATACAGGAATCCACTGAAGAACAAGACTGAAAGTACCA  
 TGTTTATATGACAGGCTTACAGATGATTTTGAGCTGCAAGTCTTCTATTTTACTATTT  
 40 TTTGCAATCTATCTTCTTACCTTGATAGGCAATTTAGGCTGGTTGTGTGGTCAATTGAGG  
 ATTCCTGGCTCCACAAACCCATGTATATTTTCTAGTGTTTATCATCTTGGATGCTTGC  
 TATCTACAGTTGTCACTCCAAAAATGTTGGTCAATTTCTGGGCAAAAAATAATCACTTT  
 CATTTATCGGATGTGCAACACAGATGCTTCTTTTGTACTTTTGGAACTACAGAATGTTT  
 45 CTCTTGGCTGCAATGGCTTATGATCATATGATGCCATCTACAACCTCTCTGTAATTCAGT  
 GAGCATGTACCCAGAGTCTATGTGCACTACTGCTCTCTACGTTGCTGGCAATTTTAC  
 ATGTCTACTACATATAGTGGCTACATTTAGGCTGTCTCTGTTGGATCCAAATGAAATAG  
 GCATGTCTTTTGTGATATGCTCTCTCTCTGCTATTTCTGTCTGACACTACACAAAC  
 AGCTCTCTACTCTTCTACTTGTGGGTTCTATGAGATAGTCACTATCTGATTGTCTCTATT  
 50 TCTGTGATTTCATTCTGTGTGCTTCTGAAAGTGTCTGCTGAAGGGAAGGCAAAAGG  
 CCTTCTCTACATGTGGCTCTCACCTAACTGGAGTGACAAATTTATCATGGAACAATTTCTCGTC  
 AGTTATATGAGACCAAGTTCAGCTATGCTTACAGACCATGACATCATAGTGTCATATTT  
 ACACAAATGTGATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAAACAAAGATGAAA  
 AAAGGCAGTGAAGAAAATGTTGAAATTGGTTTACAAATGA (SEQ ID NO: 130)



**AOLFR71 sequences:**

MGRNNNTNPVDFILTGLSDSEEVQMALFILFLIYLITMLGNVGMILIRLDLQLHTPMYFFLTH  
LSFDLSYSTVTPKTLANLLTSNYISFMGCAQMFYFVLGAABECFLSSMAYDRYVAICSPRLY  
PVIMSKRLCCALVTGPYVISFINSFVNVVMSRLHFCDNSNVVRHFCDTSPILALSCMDTYDIEI  
MIHLAGSTLMVSLITISASYVLSILTKINSTSGKQKALSTCASHLLGVTFITYGTMIFFYLPKPK  
SYSILGRDQVASVFYITIVPMLNPLIYSLRNKEVKNALIRVMQRQDQR (SEQ ID NO: 131)

ATGGGTAGAAGAAATAACACAAATGTGCTGACTTCATCCTTACGGGAGCTGTCAGATTCTG  
AAGAGGTCCAGATGGCCCTCTTTATACTATTCTCTCTGATATACCTAATTACTATGCTGGGC  
AATGTGGGATGATATGATAATCCGCTGGAGCTCCAGCTTCCACATCCCATGTATTTTT  
TCCTTACTCACTTGTCACTTTATGACCTCAGTACTCAACTGATCATCACACCTAAACACCTTA  
GCGAACTTACTGACTTCCAACATAATTTCTCTCATGGGCTGCTTTGCCAGATGTTCTTTTT  
TGCTCTCTTGGGAGCTGCTGAATGTTTTCTCTCATCAATGGCCTATGATCGCTACGTAG  
CTATCTGCAGTCTCTACGTTACCCAGTTAATATGTCCAAAAGGCTGTGTTGCGCTCTTGTC  
ACTGGGCCATGTGATTAGCTTTATCAACTCCTTTGTCAATGTGGTTTGGATGAGCAGAC  
TGCATTTCTGGGACTCAAAATGTAGTTCGTCACTTTTCTGCGACACGCTTCCAATTTTAGCT  
CTGTCTGCATGGACATACGACATCGAAATCATGATACACATTTTAGCTGTGTTCCACCC  
TGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTTCTCTTACCATCCTGAAA  
ATTAAATCCACTTCAGGAAAGCAGAAAGCTTTGTCTACTTGTGCTCTCATCTCTCTGGGAG  
TCACATCTTTTATGGAACATGATATTTTACTATTTAAACCAAGAAAGCTCTATTCTTTTG  
GGAAGGGATCAAGTGCTTCTGTTTTTATACTATTGTGATTCCCATGCTGAATCCACTCAT  
TTATAGCTTAGAAACAAAGAGTTAAAAATGCTCTATTAGAGTCATGCAGAGAAGACA  
GACTCCAGGTAA (SEQ ID NO: 132)

**AOLFR72 sequences:**

MAPENFTRVTEFILTVGVSSCPLEQIPLFLVFLVLYGLTMAGNLGIITLTSVDSRLQTPMYFFLQHL  
ALINLGNSTVIAPKMLINFLVKKTTTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL  
YMVVVSRRLLCLLVSLTYLYGFSTAIVVSSYVFSVSYCSNNIHFCYDNVPLALSCSDTYLPE  
TVVFISAAITNVVGSILIVLSYFNVLSILKICSSEGRKKAFSTCASHMMAVTFITYGTLFMYVQP  
RSNHSLEDDEKMASVFYTLVPLNPLIYSLRNKDVKTLQRFMTNLNCSFKTM (SEQ ID NO: 133)

ATGGCTCTGAAAAATTCACAGGGTCACTGAGTTTATTCTTACAGGTGTCTCTAGCTGTC  
CAGAGCTCCAGATTCCTCTCTCTGGTCTTTCTGGTGCTCTATGGGCTGACCATGGCAGG  
GAACCTGGGCATCATCACCTCACCACTGTTGACTTCGACCTCAAACCCCATGTACTTTT  
TCTGTCAACATCTGGCTCTCATTAATCTTGTAACCTCTACTGTCAATGGCCCTAAAATGCTG  
ATTAACCTTTTATGTAAGAAGAAACACTACTTCTATGAATGTGCCACCCAACTGGGAG  
GGTCTCTGTTCTTTATTGTATCGGAGGTAATCATGCTGGCTTGTGATGGCTGTGACCGCTAT  
TGGGCTATTGTAAACCTCTGCTGTACATGGTGGTGGTGTCTCGGGGGCTCTGCCTCCTGCT  
GGTCTCCCTCACATCTCTATGGCTTTTCTACAGCTATTGTGGTTTTCATCTTATGATTCT  
CTGTGCTTATTGCTCTTCAATATAATCAATCATTTTACTGTGATAATGTTCTCTGTTA  
GCATTATCTGCTCTGATACTTACTTACGAGAAACAGTTGCTTTATATCTGCAGCAACAA  
ATGTGGTGGTTCCTTGATTATAGTTCTAGTATCTTATTCAATATTGTTTGTCTATTTTA  
AAAATATGTTTCAACAGAAGGAAGGAAAAAGCCTTTCTACCTGTGCTTCACATATGATGG  
CAGTCACAATTTTTATGGGACATTGCTATTCTATGATGTGCGACGCCCAAGTAACCATTC  
ATTGGATACTGATGATAAGATGGCTTCTGTGTTTACACGTTGGTAATTCCTATGCTGAAT  
CCCTTGATCAACCTGAGGAATAAGGATGTGAAGACTGCTACAGAGATTATGATGACA  
AATCTGTCTATTCTTTAAAAACAATGTAA (SEQ ID NO: 134)

**AOLFR73 sequences:**

MNHVVVKHNHTAVTKVTEFILMGITDNPLQAPLFLGLFLIYLVTVIGNLGMVILTYLDSKLHTP  
MYFFLRLHSITDLGYSTVIAPKMLVNFVHKNTISYNWYATQLAFFEIFIISSELFILSAMAAYDRYV  
AICKPLVYVIMAEKVLVWLVIVPYLYSTFVSLFLTKLFLKLSFGCSNHSYFYCDCIPLMSILCSDT  
NELELILFSGCNLLSVLSIVLSYMFILVAILRMNSRKGRYKAFSTCISSHFVTVIMFYGTLFIYIL  
QPKSSHTLAIDKMASVFYTLIPMLNPLIYSLRNKEVKDALKRLTNRKFPI (SEQ ID NO: 135)

ATGAATCATGTGGTAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATCTCA  
 TGGGGATTACAGACAACCTGGGCTGCAGGCTCCACTGTTTGGACTCTTCCATCATATA  
 TCTGGTCACAGTGATAGGCAATCTGGGCATGGTTATCTTGACCTACTTGGACTCCAAGCTA  
 CACACCCCCATGTACTTTTCTTATAGACATTTGTCAATCACTGATCTTGGTTACTCCACTGT  
 5 CATTGGCCCGAAGATGTTAGTAACTTCATAGTGCACAAAAACAATTTCTTACAATTTGG  
 TATGCCACTCAGCTAGCATTTCTTGAGATTTTTCATCATCTCTGAGCTCTTTATTTCTATCAGC  
 AATGGCTCATGATCGCTACGTAGCCATCTGTAAACCTCTTCTGACGTGATCATGGCA  
 GAGAAAGTACTTTGGGTGCTGGTAATTTGTTCCCTATCTCTATAGCACGTTTGTGTCACATTT  
 TCTCAATAAGTTATTTAACTGTCCCTCTGTGGCTCAACAATAATCAGCTATTTTACT  
 10 GTGACTGTATCCCTCTGATGTCCATACTCTGTCTGACACAAATGAATTAGAATTAATAAT  
 TTTGATCTCTCAGGGCTGTAATTTGCTCTTCTCCCTCTCAATTTGTTCTCATATCTCATGTTT  
 TATTTAGTGGCCATCTCAGAATGAACTAAGGAAAGGGAGGTACAAAGGCTTTTCTCCACC  
 TGTAGCTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTTGTTATTTATTACTTGCA  
 ACCCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTCAGTGTTTTATACCCGTGTG  
 15 ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGATAAAGATGCTCTAA  
 AGAGAACTTTAACCAATCGATTCAAATTTCCCATTTAA (SEQ ID NO: 136)

#### AOLFR74 sequences:

MEQHNLTTVNEFILTGITDIAELQAPLFLFLMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH  
 20 LAFMDLGYSTTVGPKMLNVFVVDKNIIISYYFCATQLAFLFVFIGSELFILSAMSVDLYVAICNPL  
 LYTVIMSRVVCQVLVAIPYLCTFISLLVTIKIFLSPFCGYNVISHVFDSPLPLPCCSNTHIEILI  
 ILFAADLISLLVLVLLSYLLVAILRMNSAGROKAFSTCGAHLTVVIVFVGTLLFMYVQPKSSH  
 SFDTDKVASIFYTLVIPMLNPLIYSLRNKDVKYALRRTWNNLCNIFV (SEQ ID NO: 137)

ATGGAACAACAACATCTAACACCGTGAATGAATTCATTCTTACGGGAATCACAGATATC  
 GCTGAGCTGCAGGCACCAATTATTGTCATTGTTCTCATGATCTATGTGATCTCAGTGAATGG  
 GCAATTTGGGCATGATTTGCTCTCACCAGTGGAGTCCAGGTTGCAAAACCCCTATGTACTT  
 TTTCTCAGACAICTGGCTTTCATGGATCTGGTTATTCAACAACCTGTGGGACCCAAAATG  
 25 TTAGTAATAATTTGTTGGTGGTAAGAATAAATTTCTTATTTATTTTGGCAACACAGCTAGC  
 TTTCTTTCTGTGTTCTATGGTAGTGAACCTTTTATTCTCTCAGCATGTCTCAGCAGCTCT  
 30 ATGTGGCCATCTGTAACCCCTCTGCTATACACAGTAATCATGTCAAGCAAGGGTATGTCAAGT  
 GTGGTAGCAATCCCTTACCTTATTGACATCTTCTTCTCTCAGTACGATAAAGATTT  
 TTACTTTTACTCTTCTGGTGTACAACGTCATTAGTCATTCTTCTACTGTGACAGTCTCCCTTGT  
 TTACCTTTGCTTTGTTCAAATACACATGAAATTTGAATTGATAATTCTGATCTTTGCGAGTAT  
 35 TGATTTGATTTCACTCTCTGATAGTTCTTTATCTTACCTGCTCATCTTGTAGCCATTCT  
 CAGGATGAATTTCTGCTGGCAGACAAAAGGCTTTTCTACTGTGGAGCCCACTGACAGTG  
 GTCATAGTGTCTATGGGACTTTGCTTTTCTGTCAGCTGCAGGCCAAGTCCAGTCATTCTCT  
 TGACACTGATAAAGTGGCTTCCATATTTTACACCCCTGGTTATCCCCATGTTGAATCCCTTGA  
 TCTATAGTTTACGAAAAACAAGATGTAATAATATGCCATCGAAGGACATGGAATAACTTATG  
 40 TAATATTTTGTGTTAA (SEQ ID NO: 138)

#### AOLFR75 sequences:

MEGKNQTNISEFLLLGFSWQQQVLLFALFLCLYLTLGLFNLILLIGAIDHCLHTPMYFFLA  
 NLSLVDLCLPSATVPLKMLLNQQTQTQTSYPGCLAQMYFCMFMANMDNLLTVMAYDRYVAI  
 45 CHPLHYSTIMALRLCASLVAAPWVIAILNPLHLTLMMAHLHFCSDNVIIHFFCDINSLPLSCSD  
 TSLNQLSVLATVGLIFVVPVVCILVSYILVSAVMKVPSAQGLKAFSTCGSHLALVILFYGANT  
 GVVMSPLSNHSTEDKSAASVIFMVVAPVLNPFYSLRNELGTLKTLRSPGVAHAHCNPSL  
 GGRGWWIMSRGDRDHPG (SEQ ID NO: 139)

ATGGAAGGAAAAATCAAACCAATATCTCTGAATTTCTCTCTGCGCTTCTCAAGTTGGC  
 AACAACAGCAGGTGCTACTCTTTGCACTTTTCTGTGTCTATTAAACAGGGGTGTTTGGGA  
 AACTACTCATCTTTGCTGGCCATTGGCTCGGATCACTGCTTACACACCCCATGATTCTTCT  
 CCTTGCCAATCTGTCTTGGTAGACCTCTGCCTCCCTCAGCCACAGTCCCCAAGATGCTAC  
 TGAACATCAACAAACCAACCAACCAATCTCCTATCCCGGCTGCCTGGCTCAGATGTAATTT  
 50 CTGATGATGTTTGCCAATATGGACAATTTCTTCTCAGATGATGGCATATGACCGTTAC  
 GTGGCCATCTGTCAACCTTTACATTACTCCACCATTATGGCCCTGCGGCTCTGTGCTCTCT

GGTAGCTGCACCTTGGGTCATTGCCATTTTGAACCCCTCTCTGCACACTCTATGATGGCCCC  
 ATCTGCACCTCTGCTCTGATAATGTTATCCACCATTCTCTGTGATATCAACTCTCTCCTC  
 CCTCTGTCTGTTCCGACACCCAGTCTTAATCAGTTGAGTGTCTGGCTACGGTGGGGCTGA  
 TCTTTGTGGTACCTTCAAGTGTGATCCTGGTATCCTATATCCTCAITGTTTCTGCTGTGATG  
 5 AAAGTCCCTCTCGCCAAAGGAAAACCAAGGCTTTCTACCTGTGGATCTCACCTTGCCCTT  
 GGTCACTCTTTCTATGGAGCAAAACAGGGGCTATATGAGGCCCTTATCCAATCACTCT  
 ACTGAAAAAGACTCAGCGCATCAGTCAATTTATGGTTGTAGCACTGTGTTGAATCCAT  
 TCATTACAGTTTAAGAAACAATGAACCTGAAGGGGACTTTAAAAAAGACCTTAAGCCGGC  
 CGGCGCGGTGGCTACGCCGTGTAATCCAGCACTTTGGGAGCGCGAGGCGGGTGGATCA  
 10 TGAGGTGAGGATGAGACCATCTCGGCTAA (SEQ ID NO: 140)

#### AOLFR76 sequences:

MENNTVESEFILLGLTNAPELQVPLFIMFTLIYLITLGNLGMILLILLSHLHTPMYFFLSNLSLA  
 GIGYSSAVTPKVLTLGLLIEDKAISYSACAAQMFFCAVFAVTENYLLSSMAYDRYAACVNPPLHY  
 15 TTTMTTRVCACLAIGCYVIGFLNASIQIGDTRLSFCMSNVIIHFFCDKPAVITLTCSEKHSIL  
 VLISSENFV FALLVTLLSYLFILITLKRHTGKGYQKPLSTCGSHLIAIFLYITVIHMYRPSSSHSM  
 DTDKIASVFTMIIPMLSPIVYTLRNKDVKNAPMKVVEKAKYSLDSVF (SEQ ID NO: 141)

ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCCTGGTCTAACCAATGCCCCAGAA  
 20 CTACAGAGTCCCTCTTTATCATGTTTACCCCTCATCTACCTCATCACTCTGATCGGGAACT  
 GGGGATGATCATATTAATCTGCTGGACTCTCATCTCCACACTCCCATGTACTTTTTCTCA  
 GTAACTCTGTCTCTGCAGGCATTGGTTACTCTCAGCTGTCACTCCAAAGGTTTAACTGG  
 GTTGCTTATAGAAAGCAAAAGCCATCTCTACAGTCCGTGCTCAGATGTCTTTTGT  
 25 GCAGTCTTTGCCATCTGGGAAAAATACCTCTTGCTCTCAATGGCCTATGACCGCTACGCAG  
 CAGTGTGTAACCCCTACATTATACCACCACTGACAAACAGTGTGTGCTGTCTGTGCG  
 TATAGGCTGTATGTCAATGGTTTCTGAATGCTTCTATCCAAATGGAGATACATTTCGCC  
 TCTCTTCTGCATGTGCCAATGTGATTCATCACTTTTCTGTGACAAACAGCATCACTTCT  
 CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATTCTTGTTCTTATATCAAGTTTAAATGT  
 30 CTTTTTGCACCTTGTGTTACCTTGATTTCCTATCTGTTCAATATGATCACCATTCTTAAGAG  
 GCACAGCGTAAGGGATACCAGAAAGCCTTTATCTACCTGTGGTTCTCACCCTCATGGCAAT  
 TTCTTATTTTATAATACTGTATCATATGATACACGACCAAGTCCAGTCTTCCATGGA  
 CACAGACAAAATGTCATCTGTGTTCTACACTATGATCATCCCCATGCTCAGTCTTATGCT  
 ATACCTGAGGAACAAAGACGTGAAGAATGCATTTCATGAAGTGTGTTGAGAAGGCAAAAT  
 35 ATTTCTAGATTCACTTTTAA (SEQ ID NO: 142)

#### AOLFR77 sequences:

MGDVNSQSVASDFILVGLFSHSGSRQLLSLVAVMVFVIGLLGNTVLLFLIRVDSRLHPTMPLYLLS  
 QLSLFDIGCPMVTIPKMASDFLRGEGATSYGGGAAQIFLLTMGVAAEGLVLLVMSYDRYVAVC  
 40 PQLQYVPLMRRQVCLLMMGSSVVVGVNLNASIQTSITLHFPYCASRIVDHFFCEVPALLKLSCA  
 DTCAYEMALSTSGVILMLPLSLIASYGHVLQAVLSMRSEARHKAVTTCSHITVVLGFLVGA  
 AVFMYMVPYCAHYSPQQDNVVSIFYSLVPTPLNPLYSLRNPEVWMALVKVLSRAGLRQMC  
 (SEQ ID NO: 143)

ATGGGGGATGTGAATCAGTCGGTGGCCCTCAGACTTCATTCTGGTGGGCCTCTTCAGTCACT  
 45 CAGGATCAGCGCAGCTCTCTCTCCTCGTGGCTGTCAATGTTGTGTCATAGGCCCTCTGGGC  
 AACACCGTTCTCTCTCTGATCCGTGTGGACTCCCGGCTCCACACACCATGACTTCTCT  
 GCTCAGCCAGCTCTCCCTGTTTGACATTGGCTGTGCCATGGTCACCATCCCAAGATGGCA  
 TCAGACTTCTGCGGGGAGAAGGTGCCACCTCCTATGGAGGTGGTGCAGCTCAAAATATCT  
 50 TCCTCAACATGATGGGTGTGGCTGAGGGGCTCTGTGTGTCCTCATGCTTATAGACCGTTA  
 TGTGTGTGTGTGACCAAGCCCTGCAGTATCTGTACTATGAGACGCCAGGATGCTGCTGT  
 ATGATGGGCTCTCTCTGGTGGTAGGTGTGCTCAACGCCCTCCATCCAGCCTCCATCAACC  
 TGCAATTTCCCTACTGTGCCCTCCCGTATTGTGGATCACTTCTCTGTGAGGTGCCAGCCCTA  
 CTGAAGCTCTCTGTGCAGATACCTGTGCCCTACGAGATGGCGCTGTCCACCTCAGGGGTGC  
 TGATCTTAATGCTCTCTTTTCCCTCATCGCCACCTCTACGGCCAGCGTGTGACAGGCTGT  
 55 CTAAGCATGCGCTCAGAGGAGGCCAGACACAAGGCTGTACCACCTGCTCTCGCATCA  
 CGGTAGTGGGGCTCTTTATGGTGCCGCCGTGTTCATGTACATGGTGCCTTGGCGCTACCA

CAGTCCACAGCAGGATAACGTGGTTTCCCTCTTCTATAGCCTTGTCACCCCTACACTCAAC  
CCCCCTATCTACAGTCTGAGGAATCCGGAGGTGGATGGCTTTGGTCAAAGTGCTTAGCA  
GAGCTGGACTCAGGCAAATGTGCTGA (SEQ ID NO: 144)

5 **AOLFR78 sequences:**

MSPDGNHSSDPTFVLAGLPNLNSARVELFSVFLVYLLNLGNVLIVGVVRADTRLQTPMYF  
FLGNLSCLIEILLTSVHPKMLSNFSLRQHTISFAACITQFYFYFFLGAASEFLLAVMSADRYLAICH  
PLRYPLLMGSAVCFRVALACWVGGVLPVLGPTVAVALLPCKQGAUVVQHFFDCSGPLLRAC  
TNTKLEETDFVLASLVVSSLLITAVSYGLIVLAVLSIPASGRQKAFSTCTSHLIVVTLFYGSAI  
FLYVRPQSQSVDTNWAVTVITTFVPLNPFYALRNEQVKEALKDMFRKVVAGVGLNLLLD  
KCLSEKAVK (SEQ ID NO: 145)

ATGAGTCTGTATGGGAACACAGTAGTGATCCAACAGAGTTGCTGCTGGCAGGGCTCCCA  
AATCTCAACAGCGCAAGAGTGGAATTATTTTCTGTGTTTCTTCTGTGCTATCTCTGTAATCT  
GACAGGCAATGTGTTGATTGTGGGGGTGGTAAGGGCTGATACTCGACTACAGACCCCTAT  
GTACTTCTTTCTGGGTAACCTGTCTGCCTAGAGATACTGCTCACTTCTGTCTCATTTCCAA  
AGATGCTGAGCAATTTCTCTCAAGGCAACACACTATTTCCTTTGCTGCATGTATCACCCA  
ATTCTATTCTACTTCTTTCTCGGGGCTCCGAGTTCTTACTGTGGCTGTCAATGTCGCGG  
ATCGCTACCTGGCCATCTGTCATCCTCTGCGCTACCCCTTGCTCATGAGTGGGGCTGTGTG  
CTTTCGTGTGGCCTTGGCCTGCTGGGTGGGGGAATCTGCCCTGTGCTTGGTCCCAACAGTG  
GCTGTGGCCTTGCTTCTCTTGTGAAGCAGGGGTGCTGTGGTACAGCACTTCTTCTGCGACA  
GTGGCCCACTGCTCGCGCTGGCTTGCAACCAACCAAGAGCTGGAGGAGACTGACTTGTGT  
CCTGGCTCCCTCGTCACTTGTATCTTCTTCTGCTGATCACTGCTGTCTTCACTCGGCCATTG  
TGCTGGCAGTCTGAGCATCCCTCTGCTTCAGGCCGTGAGAAGGGCTTCTTACTCTGTAC  
CTCCCACTGTATGATGGTGACCCCTCTTCTATGGAAAGTGCCATTTTTCTCTATGTGCGGCCAT  
CGCAGATGTGGTTCTGTGGCACTAACTGGGCAGTGACAGTAATAACGACATTTGTGACAC  
CACTGTGAATCCACTCATCTATGCGCTTACGTAATGAGCAAGTCAAGGAAGCTTTGAAGGA  
CATGTTTAGGAAGGTAGTGGCAGGCGTTTAGGGAATCTTTACTTGATAAAATGTCTCAGT  
GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

30 **AOLFR79 sequences:**

MTPGELALASGNHTPVTKFILQGFSNYPDLQELLFGAILLIYAITVVGNLGMMALIFTDSHLQSP  
MYFFLNVLSFLDICYSVVTPKLLVNFVSDKSISFEGCVVQLAFFVVHVTAESFLLASMAFYDR  
FLAICQPLHYGSIMTRGTCLQLVAVSYAFGGANSIAITGNVFALPFCGPNQLTHYYCIDPPLLH  
LACANTARVVLVYFSALVTLPLAAVILTSYCLVLVAIGRMRSVAGREKDLSTCASHFLAIAI  
FYGTVVFTYVQPHGSTNNTNGQVVSFVYTHIIPMLNPFYSLRNEKVGALQRKLQVNIFFG  
(SEQ ID NO: 147)

ATGACACCTGGAGAACTAGCCCTTGCCAGTGGCAACCAACCCAGTCACCAAGTTCACT  
TGCAGGGATTCTCAATTATCCAGACCTCCAGGAGCTTCTCTTCGGAGCCATCTCTGCTCAT  
CTATGCCATAACAGTGTGGGCAACTTGGGAATGATGGCACTCATCTTCAACAGTCCCAT  
CTCCAAAGCCCAATGTATTCTTCTCTCAATGTCCTCTCGTITCTTGATATTGTACTCTTCT  
GTGGTCACACCTAAAGTCTTGGTCAACTCTCTGCTCTCTGACAAGTCATCTCTTTTGAGG  
GCTGTGTGGTCCAGCTCGCCTTCTTGTAGTGATGTGACAGCTGAGAGCTTCTGCTGGC  
CTCATGGCCATTGACCGCTTCTAGCCATCTGTCAACCCCTCCATTATGGTCTATCATGA  
CCAGGGGACCTGTCTCCAGCTGGTAGCTGTGCTTATGCAATTGGTGAGGCCAATCCGCG  
TATCGACTGGAAATGTTCTTGGCCTGCCCTTCTGTGGGGCCCAACCAAGTCACACACTAC  
TACTGTGACATACCAACCCCTTCTCCACCTGGCTTGTGCCAACACAGCCACAGCAAGAGTGG  
TCTTCTATGCTTTTCTGCTCTGGTCAACCTTCTGCTGCTGCACTCATCTTCACTCTCTACT  
GCTTGTGCTTGGTGGGCCAATGGGAGGATGCGCTCAGTAGCAGGGAGGAGAGAAGGACCTCT  
CCACTTGTGCTCCCACTTCTGGCCATTGCCATTCTTCTATGGCACTGTGGTTTCACTAT  
GTTCAGGCCATGGATCTACTAACAATAACCAATGGCCAAAGTGTGTCGCTTCTTCAACCA  
TCATAATTCCCATGCTCAATCCCTTCTATATAGCTCCGCAACAGGAGGTGAAGGGCGC  
TCTGCAGAGGAAGCTTCAGGTCAACATCTTCCCGGCTGA (SEQ ID NO: 148)

**AOLFR80 sequences:**

MEGINKTAKMQFFRPFSPDPEVQMLIFVVFLMMYLTSLGGNATIAIVQINHSLHTPMYFFLA  
NLAVLEIFYTSSITPPLALANLNSMGKTPVSITGCGTQMFFVFLGGADCVLLVVMAYDRFIAICH  
PLRYRLIMSWSLCVELLVGLSVLGFLLSLPLTILFIHLPFCHNDEIYHFYCDMPAVMRLACADTR  
VHKTALYHSFVLISPLISLISYVVFIVAILRIRSAEGRQQAYSTCSSHLVLLQYGCSTFIYLSPS  
SSYSPEMGRVVSVAYTFITPILNPLIYSLRNKELKDALRLKALRKF (SEQ ID NO: 149)

ATGGAAGGAATAAATAAACTGCAAAGATGCAGTITTTCTTTTCGTCCATTCTCACCTGACC  
CTGAGGTCAGATGCTGATTITTTGTGGTCTTCTCTGATGATGTATCTGACCAAGCCTCGGTGG  
AAATGCTACAATGGCAGTCATTGTCAGATCAATCATCCCTCCACACCCCATGTACTTTT  
TCCTGGCTAACTGGCAGTCTAGAAATCTTCTATACATCTTCCATCAACCCCATTTGGCCTTG  
GCAAACTCCTTTCAATGGGCAAACTCCTGTTTCCATCAGGGATGTGGCACCAGATGT  
TTTTCTTTGTCTCTTGGGTGGGGCTGATTGTGTCTGCTGGTAGTCATGGCTTATGACCGG  
TTTATAGCGATCTGTCAACCTCTGCGATACAGGCTCATCATGAGCTGGTCTTGTGTGG  
AGCTGCTGGTAGGCTCCTTGGTGTGGGGTTCCTGTTGTCACTGCCACTCACCATTTTAATC  
TTCCATCTCCCATCTGCCACAATGATGAGATCTACCACCTTCTACTGTGACATGCTGCGAGT  
CATGGCCTGGCTTGTGCAGACACACGCGTTCACAAGACTGCTCTGTATATCATCAGCTTC  
ATCGTCTTATGACATCCCCCTCTCATTGATCTCCATCTCTATGTCTTCACTGGTAGCCAT  
TTTAGCGGATCGGTCAGCAGAAAGGGCGCCAGCAAGCCTACTCTACCTGCTCTTCTCACATC  
TTAGTGTCTCTCTGCAAGTATGGCTGCACAGCTTTATATCTGTCCCCAGTTCCAGCTA  
CTCTCTGAGATGGGCGGGTGGTATCTGTGGCTACACATTATCACTCCCATTTTAAAC  
CCCTTGATCTATAGTTTGAGGAACAAGGAAGTGAAGATGCCCTAAGGAAGCATTGAGA  
AAATTCTAG (SEQ ID NO: 150)

**AOLFR81 sequences:**

MGVKNHSTVTEFLSGLTEQAELQLPLFLFLGIYTVTVVGNLSMISIRLNRLHTPMYFFLSS  
LSLDFCYSSVITPKMMKLWMESHLIVPETRPSPRMMSNQTLVTEFILQGFSEHPPEYRVFLSFCF  
LFLYSGALTGNVLITLITFNPLGHAPMYFFLLNLATMDIICSSIMPKALASLVSEESSIYGGC  
MAQLYFLTWAASSELLLLLVMAVDRYAACHPLHYSSMMMSKVFCSLGATAVVLLCAVNTAIH  
TGLMLRLDFCGPNVHHFFCEVPPLLLLSCSSTVYVNGVMIVLADAFYGVNFMLTIASYGFIVSSI  
LKVKTAWGRQKAFSTCSSHLTVVCMYYTAVFYAYISPVSGYSAGKSKLAGLLYTVLSPTLNPL  
ITYLRNKEVKAALRKLFPFFRN (SEQ ID NO: 151)

ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCAGAAACCCGTCCAGCCCAAGGATG  
ATGAGTAACCGAGAGTTGGTAACCGAGTTCATCTCGAGGGCTTTTCGGAGCACCAGAAT  
ACCGGGTGTTCTTATTACAGCTGTTTCTCTCTCTACTCTGGGGCCCTCAGAGGTAATGTC  
CTCATCACTTGGCCATCAGCTTCAACCTGGGCTCCACGCTCTATGTACTTTTCTTACT  
CAACTTGGCTACTATGGACATTATCTGCACCTCTTCCATCATGCCAACGGCGTGGCAGT  
CTGGTGTGCGGAAGAGAGCTCCATCTCTACGGGGGCTGCATGGCCAGCTCTATTTCTCTCA  
CGTGGGCTGCATCTCCTCAGAGCTGCTGCTCTCACGGTTCATGGCTATGACCGGTACGCAGC  
CATCTGCCACCGCTGCATTACAGCAGCATGATGAGCAAGGTGTTCTGCAGCGGGCTGGCC  
ACACCGGTGTGCTGCTGCTGCGCGGTCAACACGGCCATCCACACGGGGCTGATGCTGCGCT  
TGGATTCTCTGTGGCCCAATGTCAATTCAATTTCTTCTGCGAGGTCCCTCCCTGCTGCTT  
CTCTCTGCACTCCCACTACGTCAACGGTGTATGATTGCTCGCGGATGCTTTCTACG  
GCATAGTGAACCTCTCTGATGACCATCGCGTCTATGGCTTCATGCTCTCCAGCATCTCTGAA  
GGTGAAGACTGCTCTGGGGGAGGCAGAAAGCCTTCTCCACCTGCTCTTCCACCTCACCCTGT  
GTGTGCATGATTACACCGCTGTCTTCTACGCTACATAAGCCGGGTCTCTGGCTACGCGT  
CAGGGAAGAGCAAGTTGGCTGCGCTGCTGTACACTGTGCTGAGTCTCACTCAACCCCTC  
CATCTATACCTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTTCCCTTCTTC  
AGAAATTA (SEQ ID NO: 152)

**AOLFR82 sequences:**

MQLNNNVTEFILGLTQDPFWKKIVFVIFLRLYLGTLLGNLLIISVKAQALKNPFFFLFYLSL  
SDTCLSTSIAPRMIVDALLKKTISFSECMQVFSSHVFGCLEIFILITAVDRYVDICKPLHYMTII  
SQWVCGVLMVAWVWGSCHSLVQIFLALSLPFCGPNVINHCDFDLQPLLKQACSEITYVNNLL

5 ATGCAACTGAATAATAATGTGACTGAGTTCACTTCTGCTGGATTGACACAGGATCCTTTT  
GGAAGAAAATAGTGTGTTGTTATTTTTCGCTCTCTACTTGGGAACACTGTGGGTAATTT  
GCTAATCATTAATTAGTGTCAAGGCCAGCCAGGCACCTAAGAAACCCAAATGTTCTTCTCCCT  
TCTACTTATCTTTATCTGTGATACTTGCCTCTCTACTTCCATAGCCCTCAGAATGATTGTGGGA  
TGCCCTTTGAAGAAAGAACACTATCTCCCTTCAGCGAGTGCATGATCCAAAGCTCTTTCATCC  
10 CATGTCTTTGGGCTGCCTGGAGATCTTTCATCCTCATCCTCACGGCTGTTGACCGCATGTGTTGGA  
CATCTGTAAAGCCCTGCACCTACATGACCATATAAGCCAGTGGGTCTGGTGTGTTTGTATG  
GCTGTGGCCTGGGTGGGATCCTGTGTGCATTCTTTAGTTCAAGATTCTTCTGCGCTGAGTTT  
GCCATTCGTGGCCCCAATGTGATCAATCACTGTTTCTGTGACTTGCAGCCCTGTGTGAAA  
CAAGCTGTGTCAAAAACCTATGTGGTTAACTCACTCTGTTTCCAAATAGTGGGGCCATTT  
15 GTGCAGTGAGTTATGTGCATGCTAATATCTCCTATGTGCATCTTCTGCAATCTCTGAGAAAC  
CACAGTGTCTGAAGTGATAAAGAAAGCACTTCCACATGTGTCTCCACATCAATTGTGGTCA  
TCTTGTCTTTGGACCTTGCAATATTATGTACACATGCCCTGCAACCGTATTCCCCATGGAT  
AAGATGATAGCTGTATTTTATACAGTTGGAACATCTTTCTCAACCCCTGATTTACACAGCT  
GAAGAATACAGAAGTGAAAAGTGCCATGAGGAAGCTTTGGAGCAAGAAATGTATCACAGA  
TGACAAAAGATAA (SEQ ID NO: 154)

# **AOLFR83 sequences:**

MGNWTAATEFVLNLFSLREVELLLLVLPLTFLLTLGNLLIISTVLSCSRLHTPMYFFLCNL  
SILDILFYSVSPKVLNGLSRDKTISFAGCTQCYFYFLLTVMSYDRYATICCPRLRYT  
25 TIMRPSVLCIGTVFVSWSVGGFSLVLFILISQLPFCGNSNIHFFCDGSLPALLACALMDMF  
MLSSMVLICVLVAYSITYIILTIVRIPSASGRKAFNTCSAHLTIVIPSIGITVFVYTPSQEYEL  
EINKIPLVLSVVTPFLNPFITYLRNDTVQGVLRDVWVRVGRVFEKRMRAVLRSLSSNKDHQ  
GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

30 ATGGGTAAGTGCAGCGGTGACTGAGTTTGTCTGCTGGGGTTTTCCCTGAGCAGGG  
AGGTGGAGCTGCTGCTCTCGGTGCTCTGCTGCCACGTTCTGTGCTGACTCTTCTGGGGAA  
CCTGCTCATCATCTCCACTGTGCTGCTGCTGCCGCCCTCCACACCCCATGTACTTCTCT  
TGTGCAACCTCTCTATCTCGGACATCCTCTTCACTCAGTCATCTCTCCAAAAGTGTGGCC  
AACTTAGGATCTAGGGATAAAACCATCTCCTTTGCCGGATGTATCACCAGTGCTATTCT  
35 ACTTTTCTTGGGCAAGTGTGAGTTCTCTGCTGACGGTCACTGTCTATGACCGTTATGCC  
ACCATCTGCTGCCCTCGCGGTACACCACCATCATGAGACCTTCTGTCTGCAATTGGGACCG  
TTGTATTCTTGGGTGGGAGGCTTCTGTCTGTGCTCTTCCAAACCATCTCATCTCCAG  
CTGCCCTTCTGTGGCTCCAATATCATTAACCACTCTTCTGTGACAGTGGACCTTCTGTGGC  
40 CCTGGCCTGTGCAGACACCACTGCCATCGAGCTGATGGATTTTATGCTTTCTTCCATGGTC  
ATCCTCTGCTGCATAGTCTCGTGGCCTATTCTATACGTACATCACTTGTGACCATGTGGC  
CATCTTCTGTGCAAGTGAAGGAAGGAAGGCCCTTAATACCTGTGCTTCCACCTGACCATA  
GTGATCATCTCTAGTGGCATCACTGTGTTATATGTATGTACTCCTCCAGAAAGAATATCT  
GGAGATCAACAAGATGCCCTTTGGTCTGAGCAGTGTGGTCACTCAATCTCAACCCCTTT  
ATATATACCTGTAGGAATGACACAGTGCAGGGAGTCTCAGGGGATGTGTGGGTGAGGGTT  
45 CGAGGAGTTTTTGAAGAAGGATGAGGCAGTGTGAGAAGCAGATATCTCTCAACAAA  
GACCACCAAGGAAGGGCTGTCTTCTCCACCATGTGTCTATTCTGTAAAGTCCAGTGT  
AG (SEQ ID NO: 156)

# **AOLFR85 sequences:**

MGAKNNVTEFVLGPFESREMQHTCFVVFLLFHVLTVLGNLLVIITNARKTLKSPMYFFLSQL  
50 SFADICYPSTIPKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY  
TAIMDCRCKGLLAGASWLAGFLHSILQTLTLVQLPCFGPNEIDNFFCDVHPLKLACADTYMV  
GLIVANSNGMISLASFILIISYVILLNLRSQSSDRRKAVSTCGSHVITVLLVLMPPMFMYIRPS  
TTLAADKLILFNVMPPLNPLIYTLRNDVKNAMRKLFRVKRSLGEK (SEQ ID NO: 157)

55 ATGGGTGCCAAGAACAATGTGACTGAGTTTGTATTTGGCCTTTTGTAGAGCAGAGAGA  
TGCACATACATGCTTTGTGTTATCTTCTCTTTCATGTGCTCACTGTCTGGGGACCTT

CTGGTCATCATCACCATCAATGCTAGAAAAGCCCTGAAGTCTCCCATGTATTTCTTCTGA  
GCCAGTTGTCTTTTGGTGACATATGTTATCCATCCACTACCATACCCAAGATGATTGCTGAC  
ACTTTTGTGGAGCAATAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTCTGCCCCA  
CTTCTTTTGGTGGCACTGAGATCTTCTCCTTACAGCCATGGCCTATGACCCGTATGTGGCC  
5 ATCTGTAGGCCCTGCACTACACAGCCATCATGGATTGCGGAAAGTGTGGCCTGTAGCGG  
GGGCCCTCTGTGTTAGCTGGCTTCTGTCATTCATCCTGCGAGACCCCTCTCACGGTTCAGCTG  
CCTTTTGTGGGCCAATGAGATAGACAACCTCTTCTGTGATGTTTCATCCCTGTCAAGTT  
GGCCTGTGCGAGACCTACATGGTAGGTCTCATCGTGGTGGCCAACAGCGGTATGATTTCT  
10 TTAGCATCCTTTTTTATCCTTATCATTTCCTATGTTATCATCTTACTGAACCTAAGAAGCCA  
GTCATCTGAGGACGGCGTAAGGCTGTCTCCACATGTGGCTCACAGTAATCATGTCCTT  
TGTGTTCTCATGCCCCCCATGTTTCATGTACATTCTGCTCCTCCACACCCCTGGCTGTGACAA  
ACTTATCATCTCTTTAAACATTGTGATGCCACCTTCTGCGAACCCCTTGTATCTATACACTAA  
GGAAACAACGATGTGAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTTAGGGG  
AGAAGTG6 (SEQ ID NO: 158)

15

#### AOLFR86 sequences:

MQLVLLMFLLVFIGNTAPAFSVTLESMDIPQNITEFEMGLSQNSEVQRVLVFFVFLIYVVTVC  
GNMLIVVTITSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECCMAQLFGAHF  
LGGVEIILLTVMAYDRYVIAICKPLHNTIMTRHLCAMLGVVAWLGGLFHSVLQLLVLWLPCF  
20 GPNVINHFACDLYPLLEVACTNTYVIGLLVANSGLICLLNFLMLAASYIVILYLSRHSADGRC  
KALSTCGAHFIVVAFVFPICIFTYVHPFSTLPIDKNMALFYGILTPMLNLIYTLRNEEVKNAMR  
KLFTW (SEQ ID NO: 159)

ATGCAATTAGTTCTATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT  
CTCAGTGACCTTGGAACTCATGGACATACCACAAAATATCACAAATTTTTCATGCTGGGG  
CTCTACACAGAATCAGAGGTACAGAGAGTCTCTTTGGTCTTTTTCGTGATCATGTATGG  
30 TCACGGTTTGTGGCAACATGCTCATTGTGGTCACTACCTCCAGCCCCAGCTGGCTTC  
CCCTGTGTAATTTTTCTGGCCAACCTATCCTTTATTGACACCTTTTATCTCTCTATGGC  
TCTTAAACCTCATTTGCTGACTCATGTATGAGGGGGAACCATCTCTTATGAGTGTCTGATG  
GCTCAGCTCTTTGGAGCTCATTTTTGGGAGGTGTTGAGATCATCTGCTCACAGTGATGG  
CTTATGACCGCTATGTGGCCATCTGTAAGCCCTGCACAAATACTACCATCATGACCAGGCA  
35 TCTGTGCCCATGCTGTAGGGGTGGCTTGGCTTGGGGGCTTCTGTCATTCATGTTTCAG  
CTCCTCCTGCTCCTTTGGTTGCCCTTCTGTGGGCCCAATGTGATCAATCATCTTGGCTGTGA  
CTTGACCTTTTGTGGAAGTTGCTGACCAATAACGTATGTCATTGGTCTGCTGGTGGTT  
GGCAACAGTGGTTAATCTGCTGTTGAACCTCTCATGCTGGCTGCTCTACATTGTTCAT  
CCTGTACTCCTTGAAGTCCACAGTGCAGATGGGAGATGCAAAAGCCCTCTCCACCTGTGGA  
40 GCCACCTCATGTGTGTGCTTGTCTTGTGCGCTGTATATTACTTATGTGCAATCCATT  
TCTACTTTACCTATAGACAAAAATATGGCATTATTTATGGTATTTCTGACACCTATGTGTAA  
TCCACTCATTTATACCCCTGAGAAATGAAGAGGTAAAAAATGCCATGAGAAAGCTCTTTACA  
TGTGTA (SEQ ID NO: 160)

#### AOLFR87 sequences:

MNNIAQLSLGFDLGPISVLQKIILLFKMYVSNCPNCAIHRKINYNTKLDQEVNNITEFI  
LLGLQNAEAKQLLFAVFLIYFLTMVDNLIVVTTTSPALDSPYVFLSFFSIDGCSSTMAP  
45 KMIFDILLTEKKTISFSGCMTQLFVEHFFGGVEIILLVVMAYDCYVIAICKPLYYLITMRQVCG  
LVLMAWVGGLFHAIQMLLIVLWLPFCGPNVIDHFICDLPLKLSCDTHVFGFLFAANSGLM  
CMLFISLITSYVLLCSQRKALSTCAFHITVVVLFVPCILVYLRPMFPIIDKAVSVFYVTVPTM  
LNLIYTLRNTVEVKNAMKQLWSQIWWNNLCD (SEQ ID NO: 161)

ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTTAGGGATTCCATCAGTGTAC  
AGAAAATAATCCTGACAAAAATTATTTTATTTGTTCAAAATGTATGTGTCAAATGCAATCC  
70 TTGTGCTATTACAGAAAAATCAATTATCCAAATACCAAACCTGGATTGTGAGCAAGTGAAC  
AACATAACGGAATTCATCTTGTCTGGCCTGACACAGAACGACAGGACGACAGAACTCTGTG  
TTGTGTTGTTTACACTCATCTACTTTCTACCATGGTAGACAACCTAATCATGTGTGTGACA  
ATCACCACGAGCCAGCCCTGGACTCCCGGTGTATTTTTTCTGTCTTCTTTCTCTTCAT  
80 AGATGGCTGCTCCTCTCTACCATGGCCCCAAAAATGATATTGACTTACTACTGAAAAG

AAAACATATTTCTTCAGTGGGTGCATGACCCAGCTCTTTGTAGAACATTTCTTTGGGGGAG  
 TTGAGATCACTTCTGCTCTGTTGATGGCCATGACTGCTATGTGGCCATCTGCAAGCCCTC  
 GTACTACCTGATCACAATGAACAGGCAGGTATGTGGCCCTCTGGTGGCCATGGCATGGGTC  
 GGGGGATTTCTTCACGCTCTGATTCAAATGCTTTTAATAGTCTGGCTGCCCTCTGTGGCC  
 CAATGTTCATTGACCATTTTCATCTGTGAOCCTTTCCCTCTGCTAAAACTCTCCTGCACTGACA  
 CTCACGCTCTTTGGACTCTTTGTTGCCGCCAACAGTGGGCTGATGTGTATGCTCATTTTCT  
 ATTTCTTATTACCTCTTACGTCCTAAATCTCTGCTACAGCGGAAGGCTCTCTCTACCTCGCG  
 CTTCCATATCACTGTAGTCGTCCTATTCTTTGTTCCCTGTATATTGGTGTACCTTCGACCCA  
 TGATCACTTCCCTATTGATAAAGCTGTGCTGTGTTTATACTGTGGTAACACCCATGTTA  
 AACCCCTTAATCTACACCTCAGAAACAGAGGTGAAAATGCCATGAAGCAGCTCTG  
 AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)

#### AOLFR88 sequences:

MWQKNQTSLADFILEGLFDDSLTHLFLSLTMVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ  
 LSLMDLMHVSTILKMATNYLSGKKSISFVGCAQHFLYLCGGAEFCFLAVMSYDRYVAICH  
 PLRYAVLNMKKVGLMMAVMSWLGASVNSLIHMAILMHFPFCGRKRVYHFYCEPFAVVKVLV  
 GDITVYETTVYISSILLLLPIFLISTSYVFLQSVIQMRSSGSKRNAFACTCGSHLTVSVLWFGACIFS  
 YMRPRSQCILLQNKVGSVFYSIHTPLNSLIYLRNKDVAKALRRVLRDRVITQCIQRLQLWLP  
 RV (SEQ ID NO: 163)

ATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGCTCTTCGATGACT  
 CCTTACCCACCTTTTCCTTTCTCCTTGACCATGGTGGCTTCCTTATTCGCGTGAGTGGC  
 AACACCTCACCATTCTCCTCATCTGCATTGATCCCACTTCATACACCAATGTATTTCTC  
 GCTCAGCCAGCTCTCCTCATGGATCTGATGATGTCTCCACAACTACCTCAAGATGGCT  
 ACCAACTCACTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCAGCACTTCC  
 TCTATTGTGTCTAGGTGGTGTGAATGTTTTCTTAGCTGTCAATGCCATGACCGCTAT  
 GTTGCCATCTGTCACTCGCTATGCTGTGCTCATGAACAAGAGGTGGGACTGTGA  
 TGGCTGTATGTGATGGTTGGGGCATCCGTGAACCTCCTAATTCACATGGCGATCTTGAT  
 GCACCTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTAGTTCCTCCAGCTGTG  
 TGAAGTTGATGTGGCGACATCACTGTGTATGAGACCAAGTGCATACAGCAGCATCT  
 CCTCCTCCTCCCATCTCCTGATTTCTACATCCTATGTCTTCATCCTTCAAAGTGTCAATCA  
 GATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTGTGGCTCCCACTCAGCGGT  
 GTTCTCTCTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGGTCCCACTGCACTGT  
 ATTGCAGAAACAAAGTTGGTTCTGTGTTCTACAGCATCAATACGCCCACTTGAATTCCTG  
 ATTTATACCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGTCTGAGGAGAGAT  
 GTTATACCCAGTGCAATCAACGACTGCAATTTGTGGTTGCCCGAGTGTAG (SEQ ID NO:  
 164)

#### AOLFR89 sequences:

MLDPSISSHTLVLSLFPQGLRKGTMWQKNQTSLADFILEGLFDDSLTHLFLSLTMVFLIAVS  
 GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTILKMATNYLSGKKSISFVGCAQHFLYLC  
 LCGAEFCFLAVMSYDRYVAICHPLRYAVLNMKKVGLMMAVMSWLGASVNSLIHMAILMHF  
 PFCGRKRVYHFYCEPFAVVKLVCGDITVYETTVYISSILLLLPIFLISTSYVFLQSVIQMRSSGSK  
 RNAFACTGSHLTVSVLWFGACIFS YMRPRSQCILLQNKVGSVFYSIHTPLNSLIYLRNKDVA  
 KALRRVLRDRVITQCIQRLQLWLP (SEQ ID NO: 165)

ATGCTGGACCCCAAGTATTTCCAGTCACACTCTTTATCTCCACTCTCTGTTTCTCAGGGATT  
 GAGAAAGGGGACAATGTGGCAGAAGAATCAGACCTCTTGCCAGACTTCATCCTTGAGGG  
 GCTCTTCGATGACTCCCTTACCCACCTTTTCCTTTCTCCTTGACCATGGTGGCTTCCTTAT  
 GTGGGTGAGTGACCAACCTCACCATTCTCCTCATGCTGATGATGCTCCAGCTCATACA  
 CCAATGTATTTCTGCTCAGCCAGCTCTCCTCATGGATCTGATGATGTCTCCACCAACCAT  
 CCTGAAGATGGCTACCACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA  
 ACCAGCACTTCCCTCATTTGTGTCTAGGTGGTGTGAATGTTTTCTTAGCTGTCAATGTC  
 CATGACCGCTATGTTGCCATCTGTCACTCCAGCTGTGCTGTGCTCATGAACAAGA  
 GTGGGACTGATGATGCTGTGCTGATGCTGTTGGGCGCATCCGTAACCTCCTAATTCACA  
 TGGCGATCTGATGCACTTCCCTTTCTGTGGGCTCGGAAAGTCTACCACTTCTACTGTGA



GTGCCAGCTGTTGTGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC  
ATCAGCAGCATCTCTCTCTCTCCCATCTCTCGATTCTACATCTCTATGTCTTCATCTCT  
CAAAAGTTGATCTTCAGATGCGCTCATCTGGGAGCAAGAGAAATGCCCTTTGCCACTTGTGGCT  
5 CCCACCTCAGCGTGGTTTCTCTTGGTTTGGTGCCTGCATCTCTCTACATGAGACCCAGG  
TCCAGTGCATCTATTGCAGAACAAAGTTGGTCTCTGTGTTCTACAGCATCATTAACGCCCA  
CATTGAATTCTCTGATTATACTCTCCGAAATAAGATGTAGCTAAGGCTCTGAGAAGAGT  
GCTGAGAGAGATGTTATACCCAGTGCAATCAACGACTGCAATTGTGGTTGCCCGAGTG  
TAG (SEQ ID NO: 166)

10 **AOLFR90 sequences:**

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFFSLGNMQNSFVTEF  
VLLGLSQPNPVQEIFVVFVLYIATVGGNMLIVVTILSSPALLVSPMYFFLGLFSLDACFSSVI  
TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL  
CGILMGVAWTGGLLSHMIQILFTQLPFCGPNVINHFMDLYPLELACTDTHIFGLMVVINSF  
15 FICINFSLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFVFCFVYTRPPSAFSLDKMA  
AIFYIILNPLNLIYTFRNFKEVKQAMRRIWNRLMVVSEKENIKL (SEQ ID NO: 167)

ATGTTCTCAATGACAACAGAAGCACTCAATAATTTGCACCTGGATGTACCAACTTGTTAA  
TGACTATGATACCAAAATGATCTGAAGCAAAATTTCTTTGTGCTCAATGTCAGACTATA  
20 CATGATCCCTGTGGAGCTTTCATCTTTCTTGGGAAACATGCAAAACCAAGCTTTGTA  
ACTGAGTTTGTCTCTGGGACTTTCAGAAATCCAAATGTTCAAGGAAATAGTATTGTGT  
TATTTTGTGTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATGTAGTAACCACTTCTC  
AGCAGCCCTGCTCTTCTGGTGTCTCCTATGACTCTTCTTGGGCTTCTGCTCTCTCGGCA  
TGGGTGCTTCTCATCTGCATCACCCCAAGATGATTGTAGACTCCCTCTATGTGACAAAA  
25 ACCATCTCTTTGAAGCTGCATGATGCAGCTCTTGTGTAACACTTCTTGTGGGGTGG  
AGGTGATGTTGCTCTCAGCCATGGCCTATGATGCTTATGTGGCCATTGCAAGCCCTTGCA  
TACTCTTCTCATGAACAGGAGGCTCTGTGCATCTGATGGGGTGAGCTGGACAGGG  
GGCCTCTTGCAATTCATGATACAAATCTTTTACTTCCAGCTTCCCTTTTGTGGCCCCAA  
TGTCATCAATCACTTATATGTGACTTGTACCCGTTACTGGAAGCTTGCCTGACTGATAC  
30 ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTATATGTCATCAAACTTCTCTGT  
TTGCTTGTCTCCTATGCTGTCTCTTGTCTCTGAGAACACACAGTCTGAAGGGCGCTG  
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTGTGATTTTGTTCTTGTCCCATGCA  
TATTTGTATATACAGACCTCCATCTGCTTTTCCCTTGACAAATGGCGGCAATATTTTAT  
ATCATCTTAAATCCGTTGCTCAATCCTTTGATTACACTTTCAGGAATAAGGAAGTAAAC  
35 AGGCCATGAGGAGAATATGGAACGACTGATGGTGGTTTCTGATGAGAAAGAAATATTA  
AACTTTAA (SEQ ID NO: 168)

**AOLFR91 sequences:**

MGNWSTVTEITLAPALLEIRISLFVVLVVTYTLTATGNITISLWIDHRLQTPMYFFLSNLSFL  
40 DILYTVTPKLLACLLEEKETISFAGCMQTYFYFFLGTVEFILLAVMSFDRYMAICDPLHYTVI  
MNSRACLLVLVGCWWGAFSLVLFPTIVTRLPYCRKEINHFFCDIAPLLQVACINTHLEKINFL  
SALVLSLAFITGYSYIISTILRIPSTQGRQKAFSTCASHITVSLAHGNSFVYVRPNQSSLD  
YDKVAAVLITVVTPLNPFYISLRNEKVQEVIRETVNRIMTLQIRKT (SEQ ID NO: 169)

ATGGGAACTGGAGCACTGTGACTGAAATCACCCCTAATTGCCTTCCAGCTCTCTGGAGA  
TCCGAATATCTCTCTCGTGGTTCTTGTGGTAACATACACATTAAACAGCAACAGGAAACAT  
30 CACTCATCTCCCTGATATGGATTGATCATCGCCTGCAAACTCCAAGTACTTCTCTCA  
GTAATTTGTCTTCTGGATATCTTATACACCACTGTCAATACCCCAAGAGTTGTGGCCTGC  
CTCTAGGAGAAAGAGAAAACCATATCTTTTGTGTTGTGATGATCCAAACATATTTTACT  
50 TCTTTCTGGGAGCGGTGGAGTTTATCCTCTTGGCGGTGATGTCTTGTGACCGCTACATGGC  
TATCTGCGACCACTGCACTACCGGTCACTGTAACAGCAGGGCCCTGCTTCTGCTGGTT  
CTGGGATGCTGGGTGGGAGCCCTTCTGTGTGTGTTTCCCAACCAATTGATGTGACAAGGC  
TACCTTACTGTAGGAAAGAAATTAATCATTTCTTGTGACATTTGCCCTCTCTCTCAGGTG  
60 GCTCTATAAATACTCACTCACTTGTGAGAAATAAATCTTCTCTCTCTGCTCTGCTCATCT  
GAGCTCCCTGGCACTCACTACTGGGTCTACGTGTACATAAATTTTACCATCTCTGCGTATCC  
55 CCTCCACCCAGGGCCGTCAGAAAGCTTTTCTACCTGTGCTTCTCACATCACTGTTGTCTCT

ATTGCCACGGGAGCAACATCTTTGTGTATGTGAGACCCAATCAGAACTCCTCACTGGATT  
ATGACAAGGTGGCCGTGTCTCATCACAGTGGTGACCCCTCTCCTGAACCCCTTTATCTA  
CAGCTTGAGGAATGAGAAGGTACAGGAAGTTGTGAGAGACAGTGAACAGAATCATGAC  
CTTGATACAAAGGAAAACCTGA (SEQ ID NO: 170)

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**AOLFR92 sequences:**

MRNGTVITFELLGFPVIQGLQTPLFIAIFLTYLTLAGNGLIATVWAEPRLIQIPMYFFLCNLSFLE  
IWYTTTVPKLLGTFVVARTVICMSCLLQAFHFVGTTEFLITIMSPDRYLITCNPLHPTIM  
TSKLLQLQALSSWVVGFTIVFCQTMLLIQLPFCGNVISHFYCDVGPSLKAACIDTSLLELLGVIA  
10 TLVLPGLSLLFMISYIYLSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK  
INLVSVLNTILTPLLNFPIYTI RNKEVKGALRKAMTCPKTGHAH (SEQ ID NO: 171)

ATGAGAAATGGCAGCAGTAATCACAGAATTCATCTGCTAGGCTTTCCTGTTATCCAAAGGCC  
TACAAACACCTCTCTTTATTGCAATCTTTCTCACCTACATATTAAACCCCTGACAGGCAATGGG  
15 CTTATTATTGCCACTGTGTGGGCTGAGCCAGGCTACAAATTCCAATGTACTTCTCCTTTG  
TAACCTGTCTTTCTTAGAAATCTGGTACACCACCAAGTCATCCCCAAACTGTAGGAAACC  
TTTGTAGTGGCAAGAAGACAGTAATCTGCATGTCTGCTGCTGCTGCGAGGCCCTTCTTCACT  
TCTTCGTGPGKACACCGAGTTCGTATCCTCACTATCATGTCTTTGTGACCGCTACCTCAAC  
20 ATCTGCAATCCCCCTTACCAACCCCAACCATCATGACCAGCAAACTGTGCTGCACTGGGCC  
TGAGCTCTCGGTGGTGGGCTTCAACATTGTCTTTGTGACAGCATGCTGCTCATCCAGTT  
GCCATTCTGTGCAATAATGTTATCAGTCATTCTTCACTGTGATGTTGGGCCAGTTTGAA  
GCGCGCTGCATAGACACCAAGCATTTTGAACCTCTGGGCGTCATAGCAACCACTCTTGTGA  
TCCAGGGTCACTTCTCTTAATATGATTCTTATATCTACATTCTGTCGCGCAATCCTACGA  
25 ATTCTCTCAGCCACTGGCCACCAAAAGACTTCTCTACCTGTGCTCGCACTGACAGTTGT  
CTCCTCGTCTACGGGGCTGTCTGTTCATGTACCAAGCCACAGCACACTCCCTCTTGA  
AGATTAATAAGGTGGTGTCTGTGCTAATACTATCTCTACCCCCCTTCTGAATCCCTTTATT  
TATACATTAGAAACAGGAGGTGAAGGGACCTTAAGAAAGGCAATGACTTGCCCAAG  
ACTGTCATGCAAAGTAA (SEQ ID NO: 172)

**AOLFR93 sequences:**

MLMNYSSATEFYLLGFPGEELHHILFAIFFFYLVTLMGNTVIIMIVCVDKRLQSPMYFFLGHL  
SALEILVTTIIVPVMWGLLLPGMQTIYLSACVQQLFLYLAVGTTEFALLGAMAVDRYVAVCN  
PLRYNIIMNRHTCNFVVLVSVWVFGFLQIWPVYVMFLQTYCKSNVNVNFFCDRGQLLKLSCN  
NTLFTFELFLMAVFVFLGSLIPTIVSNAYIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCLFLY  
35 VKPKTQAADYNWVSLMVSVVTPFLNPFIFLTRNDKIVIEALRDGVRKCCQLFRN (SEQ ID  
NO: 173)

ATGTTGATGAATTACTCTAGTGCCACTGAATTTTATCTCCTTGGCTTCCCTGGCTCTGAAGA  
ACTACATCATATCTTTTGTATATCTTCTTTTCTACTTGGTGACATTAATGGGAAACA  
40 CAGCATCATGATGTTCTGTGTGGATAAAGCTCTGCAGTCCCCATGTATTTCTCTC  
GGCCACCTCTCTGCCCCTGGGAGATCCTGGTCACAAACATAATCTGCCGTGATGCTTTGGG  
GATTGTGCTCGCTGGGATGACAGACAATATATGTCTGCCTGTGTGTCCAGCTCTTCTTGT  
TACCTTGTCTGTGGGACAAACAGAGTTTCGATTACTTGGAGCAATGGCTGTGGACCGTATG  
TGGCTCTGTCTGAACCCCTCTGAGGTACAACATCATTATGAACAGACACACCTGCAACTTTGT  
45 GGTCTGTGTGATGGTGTTTGGGTTTCTTTTCAAATCTGGCCGGCTCATGTGATGTTTC  
AGCTTACTACTGCAAAATCAAATGTGGTGAACAAATTTTTTGTGACCGAGGGCAATGTCT  
CAAACTACTCTGCAATAATACTCTTTTACGGAGTTTATCCCTCTTCTTAATGGCTGTTTTG  
TCTCTTTTGGTCTTTGATCCCTACAATTGTCTCCAACGCTACATCATCTCCACCATCTC  
AAGATCCCCTCATCTCTGCGCCGAGGAAATCCTTCTCCACTTGTGCTCCCACTTCACTGT  
50 TGTGTGATTGGCTACGGCAGCTGCTTGTCTCTACGTGAACCAACCAAGCAACGAGGCA  
GCTGATTACAATGGGTAGTTTCCCTGATGGTTTCAAGTAACTCCTTCTCAATCCTTT  
TCTTCAACCTCCGGAATGATAAAGTCATAGAGGCCCTTCGGGATGGGGTGAACCGCTGC  
TGTAACATATTCAGGAATTAG (SEQ ID NO: 174)

**AOLFR94 sequences:**

METWVWNSQSYTDGFFLLGIFSHSTADLVLSVVMVAVFTVALCGNVLLIFLIYMDPHLHTPMYFF  
LSQLSLMDLMLVCTNVPKMAANFLSGRKSISFVCGCIQIGLFVCLVSGEGLLLGLMAYDRYVA  
ISHPHLHYPLMNQRVCLQITGSSWAFGHIQGLQMVVMNFPYCGLRKVNHFCEMLSLKLKAC  
5 VDTSLFEKVFACCVFMLLFPFSIIVASYAHLGTVLQMHSAQAWKKALATCSSHLTAVTLFYG  
AAMFIYLRPRHYRAPHSHDKVASIFYTVLTPMLNPLIYSLRNREVMGALRKGDLDCRIGSQH  
(SEQ ID NO: 175)

ATGGAGACGTGGGTGAACCCAGTCTACACAGATGGCTTCTTCTCTTAGGCATCTTCTCCC  
10 ACAGTACTGCTGACCTTGCTCTCTTCCGTGGTATGGCGGTCTTACAGTGGCCCTCTGT  
GGGAATGTCCTTCTTCTCTCTCATCTACATGGGACCCACACCTTACACACCCCATGTACTT  
CTTCTCAGCCAGCTCTCCCTCATGGACCTCATGTTGGTCTGTACCAATGTGCCAAAGATG  
GCAGCCAACCTTCTGTCTGGCAGGAAGTCCATCTCCTTTGTGGGCTGTGGCATAACAATTG  
GCCTCTTGTCTGTCTTGTGGGATCTGAGGGGCTTCTGCTGGGACTCATGGCTTATGACCC  
15 CTATGTGGCCATTAGCCACCCACTTCACTATCCCATCCTCATGAATCAGAGGGTCTGTCTCC  
AGATTACTGGGAGCTCTGGGCTTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT  
AATGAATTTCCTCCTATGCTGGCTTGAGGAAGGTGAACCATTTCTCTGTGAGATGCTATCC  
TTGTTGAAGCTGGCCTGTGTAGACACATCCCTGTTTGAAGAAGGTGATATTGCTTGCTGTG  
TCTTACTGCTTCTTCTCCCAATCTCCATCATCTGGGCTCCTATGCTCACAATCTAGGACT  
20 GTGCTGCAAAATGCACCTCTGCTCAGGCGTGGAAAAAGGCCCTGGCCACTGCTCCTCCACC  
TGACAGCTGTACACCTCTTCTATGGGGCAGCCATGTTCTATCTACCTGAGGCTTAGGCATA  
CGGGGCCCCAGCCATGACAAGGTGGCTCTATCTTCTACACGGTCTTACTCCCATGCTC  
AACCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGGCACTGAGGAAGGGGCTG  
GACCGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)

**AOLFR95 sequences:**

MLGSKPRVHLIYLPASQVSTMGDRGTSNHSEMTDFILAGFRVPELHILLFLFLFVYAMILL  
GNVGMTHIMTDPRLNTPMYFFLGNLSFDIVFYSSVIEPKAMINFWSENKSISFAGCVAQFLFLFA  
LLIVTEGFLLAAMAYDRFLAICNPLIYSVQMSTRLCQLVAGSYFCGCISSVQSTMTTFLSFCAS  
30 RAVDHFGYCDSRPLQRLSCSDLFIHRMISFSLSCHILPTIIIVISYMYIVSTVLKIHSTGHHKAFST  
CSSHLGVVSVLYGAVFFMYLTPDRFPFLSKVASLCYSLVTPMLNPLIYSLRNKDQVQALKKFLLE  
KKNIL (SEQ ID NO: 177)

ATGCTAGGATCCAAACCAAGAGTTCAATTGTATATTTGCCCTGTGCCCTCTCAACAGGTTTC  
35 TACCATTGGGTGACAGGGGAACAAGCAATCACTCAAGAAATGACTCATCTTCTTCTGCAGG  
CTTCAAGGTACGCCACAGAGCTCCACATTTCTCTTCTTCTGCTATTGTTGTTTATGCCA  
TGATCCTCTTAGGGAATGTTGGGATGATGACCAATTATTATGACTAGTCTCCGCTGAACAC  
ACCAATGTATTITTTTCTAGGCAATCTCTCTTCTTATGATCTTTTCAITTCATCTGTATTGA  
ACCCAAGGCTATGATCAACTTCTGGTCTGAAACAAAGTCTATCTCCTTTGACAGGCTGTGTG  
40 GCCAGCTCTTCTTCTTGGCCCTCCTATTGTGACTGAGGGAATTCTCCTGGCGGCCATGGC  
TATGACCGCTTATTGCCATCTGCAACCTCTGCTCTACTCTGTGCAAAATGTCCACACGTC  
TGTGTACTCAGTGGTGGCTGGTCTTCTATTTTGTGGCTGCATTGACTCAGTATTACAGACT  
AGCATGACATTACTTATCTTTTGGCGTCTCTCGGGCTGTGACACCTTTTACTGTGATTC  
TCGCCACTCAGAGACTGCTTGTCTGATCTCTTATCCATAGAAATGATATCTTTTCTCT  
45 TATCATGTATTATTATCTTGCTTACTATCATAGTCAATTATAGTATCTTACATGTATATTGTG  
TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCCTTCTCCACTGCAGCT  
CTCACCTGGAGTTGTGAGTGTGCTGTATGGTGCTGCTTTTATGTATCTCACTCTGAC  
AGATTCTCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCCATGTGTA  
ATCCTTTGATTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAAATTTCTAGA  
50 GAAGAAAAATATTATCTTTGA (SEQ ID NO: 178)

**AOLFR96 sequences:**

MICENHTRVTEFILLGFTNNPEMQVSLFIFFLAITYVTLLGNFLIVTVTSVDLALQTPMYFFLQN  
LSLLEVCTFLVMVPKMLVDLVSPRKIISFVCGCTQMYFFFFFGSSECLLSSMAYDRFVAICNP  
55 LHYSVIMNRSCLWMAIGSWMSGVPVSMILQTAWMMALPCGPNADVHFFCDGPPVLKLTVT  
DTTMVEMQALASTLLFIMFFPCLILVSYTRIITILRMSSATGRQKAFSTCSSHLIYVSLFYGTASL

TYLRPKSNQSPESKKLVSLSYTVITPMLNPIHYGLRNNEVGAVKRITITQVKVLQKLDVF (SEQ  
ID NO: 179)

- 5 ATGATCTGTGAAAAATCACACCAGAGTCACTGAATTTATCTTCTTGGTTTTACAAACAACC  
CCGAGATGCAAGTTTCCCTCTTATTTTCTTCTGGCCATTATACAGTCACTTGTGTGGGC  
AACTTCTTATTGTACAGTTACCAAGTGTGGATTCGCACTTCAAAACCCATGTACTTCTT  
TCTTCAAAATCTGTCACTCTTGAAGTATGTTTCACTTGGTTATGGTGCCAAAATAGCTCTG  
TAGATCTAGTGTCCCAAGGAAAATATCTCTTTGTGGGCTGTGGTACCCAGATGTACTT  
10 CTTCTTCTTCTTGGCAGTCTGAATGTTTCTTCTCCATGATGGCTTATGATCGCTTGT  
GGCCATCTGTAAACCTCTCCATTATTCAGTCATAATGAACAGGGCCCTATGCTTGTGGATG  
GCCATAGGCTCTGGATGTCCGGTGTCTCTGTGTCTATGCTACAGACAGCTTGGATGATGG  
CCCTTCTTCTTGTGGACCAATGCGCTGGACCACTTTTCTGTGATGGTCCCCAGTGITA  
AAACTAGTCACAGTGGATACAACCATGTATGAAATGCAAGCACTTGCCTCCACACTCTGT  
15 TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCTACACCCGATTATCATCAACTCTG  
AGGATGTCCTCTGCCACTGGCCCGCAGAGGCCATTCTTACTGTCTCTCACACCTCATTGT  
GGTGTCCCTCTTACGGAACAGCCAGTCTGACCTACCTGCGGCCCAAAATCAAAACAGTCC  
CTGAGAGCAAGAAGCTAGTGTCTATTGTCTACAGTGCATCACACCTATGCTAAACCCCA  
TCATCTACGGCCTGAGGAACAATGAAAGTGAAGGGGCTGTCAAGAGGACAATCACTCAAA  
AAGTCTTACAGAAGTTAGATGTGTTTGA (SEQ ID NO: 180)

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**AOLFR97 sequences:**

- MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSMFVVPFSIAEHWRMKGANLSQGMFEFL  
LGLTDPQLRLLFPVFLGMYTATLLGNLVMFLIHVSATLHTPMYSLKLSFLDFCYSTTVV  
PQLTVNFLAKRKVISYFGCMTQMFFYAGFATSECYLIAAMAYDRYAICNPALLYSTIMSPVVC  
25 ASLIVGYSAGFLNSLIHTGCIIFSLKFCGAHVVTTHFFCDGPPILSLSCVDTSLEILLFIAGFNLLS  
CTLTILISYFLIILNTILKMSSAQGRKAFSTCASHLTAICLFFGTTLFMYLPRSSYSLTQDRIVA  
VIYTVVIPVLNPLMYSRLNRKDVKKALKIVWGRKTIME (SEQ ID NO: 181)

- 30 ATGACAGAGTTTTCATCTGCAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAGGCTGT  
CCTTAGGCAGAAATTAACAGCCAGTCAGAGCCCAAGGTGTTCAACCTCATTTATAGTGTGGCC  
TCTTCTTCCATGCGAGCACTGGGAGAAGGATGAAAGGGGCAAACTGACAGGGATAGGGAT  
GGAGTTTGAGCTCTTGGGCCACCACTGACGCCCAAGCTCCAGAGGCTGCTTCTGTGGTG  
TCTCTGGGCATGTACACAGCCACTCTGCTGGGGAACCTGGTCATGTTCTCTCGATCCATG  
35 TGACTGCCACCTGCACACACCCATGTACTCCCTCTGAAAGAGCTCTCTCTTGGATTTC  
TGCTACTCTCCAGCGTTGTGCCCCAGACCTGGTGAACCTTCTGGCCAAAGAGGAAAGTGA  
TCTCTATTTTGGCTGCATGACTCAGATGTTCTTCTATGCGGGTTTGGCCACAGTGAGTGC  
TATCTCATCGCTGCCATGGCCTATGACCCGCTATGCCGCTATTGTGAACCCCTGCTCTACT  
AACCATCATGTCTCTGAGGTCTGTGCTCGCTGATTTGTGGGCTCTACAGTGCAGGATTC  
CTCAATTTCTCTTATCCACACTGGCTGTATCTTTAGTCTGAAATTTCTGCGGTGCTCATGCT  
40 CACTCACTTCTTCTGTGATGGGCCACCCATCGTCTGCTGTGTTGTGTAGACACCTCACTGT  
GTGAGATCTGCTCTTCAATTTTGTGGTTCACACCTTTTGAAGTGCACCCCTCACCCTCTGT  
ATCTCTCACTTCTTAATTTCAACACCATCCTGAAAATGAGCTCGGCCAGGGCAGGTTTA  
AGGCATTTTCCACCTGTGCATCCCACTCACTGCCATCTGCTCTTCTTGGCAACAACATTT  
TTTATGTACCTGCGCCCAAGGTCCAGTACTCTTGAACCCCTCATGTACTCTTTGAAAACAAGGATGT  
45 TCTACACAGTGGTGATCCCACTGCTGAACCCCTCATGTACTCTTTGAAAACAAGGATGT  
GAAGAAAGCTTTAATAAAGGTTTGGGGTAGGAAAAACAATGGAATGA (SEQ ID NO: 182)

**AOLFR98 sequences:**

- MRGFNKTIVVTQFILVGFSSLGELQLLLFVIFLLLYLTILVANVTIMAVIRFSWTLHTPMYGFLLI  
LSFSESCYTFVIPQLLVHLLSDTKTISFMACATQLEFFLGFACNCLLIAMVGYDRYVAICHPLR  
YTLINKRLGLELISLGATGFFIALVATNLICDMRFCCGPNRNVNHYFCDMAPVIKLACTDTHVKE  
15 LALFSLVIMVPLLSLITISYGFIVNTILKIPSAEGKKAFTVCASHLTVFVHYGCASIIIVLRPKSK  
SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVKTALKRVLGMPVATKMS (SEQ ID NO: 183)
- 55 ATGCGAGGTTTCAACAAAAACCACTGTGGTTACACAGTTCATCTGGTGGGTTTCTCCAGCC  
TGGGGGAGCTCAGCTGCTGCTTTTGTCTATCTTCTTCTCTATACTTGACAACTCTGGTG

5 GCCAATGTGACCATCATGGCCGTTATTCGCTTCAGCTGGACTCTCCACACTCCCATGTATG  
 GCTTTCTATTACCTTTTCATCTTTCTGAGTCTGCTACACCTTTTGTCATCATCCCTCAGCTGC  
 TGGTCCACCTGCTCTCAGACACCAAGACCATCTCCTTCATGGCCTGTGCCACCCAGCTGTT  
 CTTTTCTCTGGCCTTGTCTGCACCACTGCCCTCCTCAITGGCTGTGATGGGATATGATCGCT  
 10 ATGTAGCAATTTGTGACCCCTCTGAGGTACACACTCATATAACAAAGGCTGGGGTTGGA  
 GTTGATTTCTCTCTCAGGAGCCACAGGTTTCTTTATTGCTTTGGTGCCACCAACCTCATTT  
 GTGACATGCGTTTGTGGGCCCAACAGGGTTAACCACTATTCTGTGACATGGCACCTGT  
 TATCAAGTTAGCGTGCATGACACCCATGTGAAAGAGCTGGGCTTTATTAGCCTCAGCATC  
 CTGGTAATTAAGTGGCTTTTCTGTAAATCTCATATCCTATGGCTTCATAGTTAAACACCAT  
 15 CCTGAAGATCCCTCAGCTGAGGGCAAGAAGGCTTTGTACCTGTGCCTCAGCATCTCACT  
 GTGGCTTTGTGCCATATGGCTGTGCCTCTATCATCTATCTGCGGCCAAGTCCAAGTCTGC  
 CTCAGACAAGGATCAGTTGGTGGCAGTGACCTACACAGTGGTTACTCCCTTACTTAACTCT  
 CTGTCTACAGTCTGAGGAACAAAGAGGTAAGAACTGCATTGAAAAGAGTTCTTGGAAATG  
 CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)

**AOLFR99 sequences:**

20 MERVNTVVRVIFLGFSSRLARLQQLFVIFLLLYLFTLTGNAIIISTIVLDRALHIPMYFFLAILSC  
 SEICYTFIIVPKMLVDLLSQKKIISFLGCAIQMFSFLFLGCSHSELLAVMGYDRIYAIENPLRYSV  
 LMGHGVCMGLVAAACACGFTVAQHTSLVFHLPFYSSNQLHHFFCDIAPVLKLASHNHFSQIV  
 IFMLCTLVLAIPLLILVSYVHLSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASHYLRPQSNY  
 SSSQDALISVSYTIITPLFNPMIYSLRNKEFKSALCKIVRRITISLL (SEQ ID NO: 185)

25 ATGGAGCGGGTCAATGAGACTGTGGTGAGAGAGGTCATCTTCTCGGCTTCTCATCCCTGG  
 CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCTGCTCCTCTACCTGTTCACCTCTGGGCACC  
 AATGCAATCATCATTTCCACCATTTGCTGGACAGGGCCCTTCATATCCCATGTACTTCT  
 CTTGCGCATCTCTCTTGTCTGTGAGATTGCTACACCTTCATCATATTGACCCAAAGATGTGG  
 TTGACCTGCTGTCCAGAAAGAACCTTTCTTCTGGGCTGTGCCATCCAAAGTGTTTCTC  
 TTCTCTTCTTGGCTGTCTCTCACTCTTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT  
 30 AGGCATCTGTAACCCACTGCGCTACTCAGTGCTAATGGGACATGGGGTGTTGATGGGACTA  
 GTGGCTGTGCTGTGCTGTGGCTTCACTGTGACAGATCATACATCCTTGGTAATTICA  
 CCTGCCCTTTTATTCTCCAATCAACTACATCACTTCTTGTGACATTTGCTCCTGTCTCA  
 AGCTGGCATCTCACCATAACCCTTTAGTCAGATTTGTCATCTCATGCTCTGTACATTTGGTC  
 CTGGCTATCCCTTATTGTTGATCTTGGTGTCTATGTTACATCCTCTCTGCCATCACTCA  
 35 GTTTCCTTCCACACTGGGTAGGTGCAAGCTTTTCTACCTGTGTATCTCACTCAATTAATTG  
 TCACTGTCCACTATGGCTGTGCCTCTTTATCTACTTAAGGCTCAGTCCAACCTACTCTCA  
 AGCCAGGATGCTCTAATATCAGTATCTACACTAATTATACTCCATTGTTCAACCAATGA  
 TTTATLVDAGTTGAGAAATAAAGAGTTCAAATCAGCTCTTTGTAAAAATTGTGAGAAACAAT  
 TTCCTGTGTGTA (SEQ ID NO: 186)

**AOLFR101 sequences:**

40 MDTGNWSQVAEPIILGFPHLQGVQIYFLLLLLLIYLMTVLGNLLFLVCLDSRLHTPMYHFVSI  
 LSFSELGYTAATIPKMLANLLSEKKITISFSGCLQIYFHLGATECYLLTAMAYDRYLACRPL  
 HYPILMTPLCAEIAIGCWGLGAGPVVEISLISRLPFCGPNRIQHVCFDPFVLSLACTDTSINV  
 45 LVDFVINSCKILATLFLILCSYVQICTVLRIPSAAGKRKAISTCASHFTVVLIFYGSILSMYVQLK  
 KSYSLVDQALAVVYSVLTPLFNPIYSLRNKEIHAVERRLQKIRIGLA (SEQ ID NO: 187)

50 ATGGACACAGGGAACCTGGAGCCAGGTAGCAGAATTCATCATCTTGGGCTTCCCCATCTCC  
 AGGGTGTCCAGATTTATCTCTTCTCTTGTGTCTTCAATTAACCTCATGACTGTGTGGGA  
 AACCTGCTGATATCTCTGGTGGTCTGCTGGACCTCCGGCTTCACACACCACTGTACCACCT  
 TGTGACAGATTTCTCTCTCAGAGCTTGGCTATACAGCTGCCACCACTCCCTAAGACTGTG  
 GCAAACCTTGCTCAGTGAGAAAAAGACCAATTTCAATCTCTGGGTGTCTCTGCAGATCTATT  
 TCTTTCACTCCTTGGAGCGACTGAGTGCTATCTCTGACAGCATATGGCTACGATAGGTA  
 TTTAGCCACTGTCCGGCCCTCCACTACCAACCCCTCATGCCCAACACTTTGTGCGAGAG  
 ATTGCCATTTGGCTGTGGTGTGGGAGGCTTGGCTGGGCCAGTAGTGAATTTCTCTTGATTT  
 55 CACGCTCCCACTTCTGTGGCCCAATCGCATTCAGCACGCTCTTTGTGACTTCCCTCTGTG  
 CTGAGTTTGGCTTGCACTGATACGCTATAAATGTCTAGTAGATTTGTTATAAATCTCTG



**AOLFR105 sequences:**

- MQQLNHTSVSEFILVGFSAFPHLQLMLFLLFLMYLFTLLGNLLIMATVWSERSLHMPMYLFLC  
ALSITEILYTVAIIPRMLADLLSTQRSIAFLACASQMFFSFGFTHSFLTLVMGYDRYVAICHPL  
RNVNVLMSLRGCTCRVGCWSAGGLVMGMVVTSAIFHLAFCGHKEIHFFCHVPPLLKLACGGD  
5 VLVVAKGVGLVCTIALLGCFLLILLSYAFIVAAILKIPSAEGRNKAFASTCASHLTVVVHYGFAS  
VYILKPKGPQSPGDTLGMITYTVLTPFLSPIIFSLRNKELKVMAMKTCFTKLPQNC (SEQ ID  
NO: 193)
- ATGCAGGGGCTAAACCAACCTCCGTGCTGAATTCATCTCGTTGGCTTCTCTGCCTTCC  
10 CCACCTCCAGCTGATGCTCTTCTGCTGTTCTCTGATGTACCTGTTACGCTGTGCGGGCA  
ACCTGCTCATCATGGCCACTGTCTGGAGCGAGCGCAGCCTCCACATGCCCATTGACTCTT  
CCTGTGTGCCCTCTCCATCACCAGAGATCCTCTACCCGTGGCCATCATCCCGCGCATGCTG  
GCCGACCTGCTGTCCACCCAGCGCTCCATCGCCTCTCTGGCCTGTGCCAGTCAGATGTTCTT  
CTCCTTCAGCTTCGGGCTTACCACACTCCTTCTGCTCACTGTGATGGGCTACGACCGCTACG  
15 TGGCCATCTGCCACCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGACCTGCCG  
GGTGGGCTGCTCTGGGCTGTTGGCTTGGTCATGGGGATGGTGGTGACCTCGGCCATTTC  
CACTCGCCTCTGTGGACACAAGGAGATCCACCATTTCTCTGCCACGTGCCACCTCTGTT  
GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTTGGTGTGAT  
CATCGGCCCTGCTGGGCTGTTTCTCTCATCTCTCTCTCATGCTTCATCGTGGCCGCCA  
20 TCTTGAAGATCCCTTCTGCTGAAGGTGCGGAACAGGCGCTTCTCCACCTGTGCCCTCTCACT  
CACTGTGGTGGTGTGCACTATGGCTTTCCTCCGTCACTTATACCTGAAGACCAAAAGGTGCC  
CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACCTACACGGCTCACTCAACCACTCTCTCA  
GCCCATCATCTTCAGCCTCAGGAACAAGGAGCTGAAGGTGCCCATGAAGAAGACTTGCTT  
CACCAAACCTTTCCACAGAAGTGTGA (SEQ ID NO: 194)

25

**AOLFR106 sequences:**

- METANYTKVFETVLTLGSLQTEPVQLVLFVIFLSFYFILPGNILICTISLDPHLTSPMYFILLANLA  
FLDIWYSSITAPEMLIDFFVERKIISFDGCIQLFLHFAAGSEMFLITVMAFDLYTAICRPLHYA  
TIMNQRLLCCLVALSWRGGFIHSIQVALIVRLPFCGPNELDSYCFDITQVVRACIANTPPEELVM  
30 ICSSGLSVVCLIALMSYAFLLALFKKLSGSGENTNRAMSTCYSHITVLMFSGPSITYARFPD  
SFSLDKVVSVFNTLIFLRLNPHIYTLRNKEVKAAMRKLVTKYILCKE (SEQ ID NO: 195)
- ATGGAACATGCAAAATTACACCAAGGTGACAGAAATTGTCTCACTGGCCTATCCAGACTC  
CAGAGGTCCAACATAGTCTCTATTGTATATTTCTATCCTTCTATTGTTCATCTACCAGGA  
35 AATATCTTATCACTTTGCACCATCAGTCTAGACCCATCTGACCTCTCCTATGTAITTCCT  
GTTGGCTAATCTGGGCTTCTTGATATTGGTACTCTCCATTACAGCCCTGAAATGCTCA  
TAGACTCTTTGTGGAGAGGAAGATAATTCTTTGTATGGATGCATTCACAGCTCTTCTT  
CTTACACTTTGTGGGGCTTCGGAGATGTTCTTGCTACAGATGACGTGGCCTTTGACCTCTACA  
CTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCAACGTCTCTGCTGTATCCTG  
40 GTGGCTCTCTCTGTGGGGGGGCTTCATTCACTTCTATCATACAGGTGGCTCTCATTTGTC  
GACTTCCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTGTG  
CCGATTGCTGTGCGCAACCTTCCAGAGGAGTGTAGTGATGATCTGTAGTAGTGTGCTGT  
ATCTCTGTGGTGTGTTTGATTGCTCTGTTAATGTCCTATGCCTTCTCTGCGCTTGTTCGAA  
AAAACCTTTCAGGCTCAGGTGAGAAATACCAACAGGGCCATGCTCCACTGCTATTCCCAATT  
45 GAAATTTGGGTGCTAATGTTTGGGCCATCCATCATATTGCTGCCCATTTGACTCGTT  
TTCCCTAGATAAAGTGGTGTCTGTGTCAATACTTTAATATTCCCTTTAAGTAATCCCAATTA  
TTTACACATTGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGTTGTCACCAATATA  
TTTTGTGTAAGAGAAAGTGA (SEQ ID NO: 196)

50

**AOLFR107 sequences:**

- MELWNFTLGSFGILVGLNDSGSPELLCATITILYLLALISNGLLLAITMEARLHMPMYLLGQ  
LSLMDLLFTSVVTPKALADFLRRENTISFGGALQMFALTMGGAEDLLAFMAYDRYVAICH  
PLTYMTLMSRRACWLMVATSWILASLALIYTVYTMHYPCRAQEIRHLLCEIPHLKLVACAD  
TSRYELMVYVMGVFTLIPLSAAILASYQILLTVLHMPSNEGRRKKALVTCSSHLTVGMFGYGA  
55 ATFMVYLPSSFHSRQDNIIISVFYITVTPALNPLYSLRNKEVMRALRRVLGKMYLPAHSTL  
(SEQ ID NO: 197)

ATGGAGCTCTGGAACTTCACCTTGGGAAGTGGCTTCATTTTGGTGGGGATTCTGAATGACA  
 TGGGGTCTCCTGAACTGCTCTGTGCTACAATTACAATCCTATACCTTGTGGCCCTGATCAG  
 CAATGGCCCTACTGCTCCTGGCATATCACCATGGAAGCCCGGCTCCACATGCCCATGTACCTC  
 5 CTGCTTGGGACGCTCTCTCATGGACCTCTGTTACATCTGTTGTACATCCCAAGGCCCT  
 TGGCGAATTTCTGCGCAGAGAAAAACCATCTCCCTTGGAGGGCTGTGCCCTTCAGATGTTC  
 CTGGCAGTGACAATGGGTGGTCTGAGGACCTCCTACTGGCCTTCATGGCCATGACAGGT  
 ATGTGGCCATTGTCACTCTGACATACAATGACCTCATGAGCTCAAGAGCCCTGCTGGCT  
 10 CATGTGGGCCACGCTCTGGATCCTGGCATCCCTAAGTGGCCATAATATACCGTGTATACC  
 ATGCACTATCCCTTCTGCAGGGCCAGGAGATCAGGCATCTCTCTGTGAGATCCCAACT  
 TGCTGAAGGTGGCCTGTGCTGATACCTCCAGATATGAGCTCATGTGATATGTGATGGGTGT  
 GACCTCTCTGATTCCTCTCTTGTGCTATACCTGGCCTCTATACACAAATCTTACTCACTG  
 TGCTCCATATGCCATCAAAATGAGGGGAGGAAGAAAGCCCTGTGACCTGTCTTCCCACT  
 15 GACTGTGGTGGGATGTCTATGAGGCTGCCACATCATGTATGTCTTGCCCACTCTCTTC  
 ACAGCACCAGACAAGACAACATCATCTCTGTTTCTACACAATTTGTCATCTCCAGCCCTGAA  
 TCCACTCATCTACAGCCTGAGGAATAAGGAGGTGATGCGGGCCTTGAGGAGGGTCTGGG  
 AAAATACATGCTGCCAGCACATCCACGCTCTAG (SEQ ID NO: 198)

**AOLFR108 sequences:**

MCSEFLCQTKGAKISMGEENQTFVSKFIFLGLSQDLQTLFILFLIYLLTVLGNQLIILIFLD  
 20 SRLHTPMYFFLRNLPSFADLCFSTISVPQVLVHFLVKRKTISFYGCMQIIVFLVGGCTECALLAV  
 MSYDRYVAVCKPLPYSTIMTQRVCLWLSFRSWASGALVSLVDTSTFHLPLYWGQNNIHYCE  
 PPALLKLASIDTYSYMAIFSMGVVILLAPVSLILGSYWNISTVIQMQSGEGRKLFSTCGSHLI  
 25 VVFLYVSGIFTYMRPNSKTTKELDKMISVFYTAVTPMLNPHIYSLRNDKVKGALRKLVRKRC  
 FSHRQ (SEQ ID NO: 199)

ATGTGTTCTTTTCTTGTGCCAAACAGGTAACAGGCCAAAAATATCAATGGGAGAGAAGAA  
 ACCAAACCTTTGTGTCCAAGTTTATCTTCTGGGTCTTTCACAGGACTTGACAGCCAGAT  
 CCGTGTATTTATCTCTTTCTCATATTTATCTGCTGACCGTGCTTGAAACACAGCTCATCA  
 30 TCTATCTCATCTTCTGGATTTCTCGCCTTCACACTCCCATGTATTTTCTTAGAAATCTCT  
 CCTTTGCAGATCTCTGTTCTCTACTAGCATTGTCCCTCAAGTGTGGTTCACCTTCTGGTA  
 AAGAGAAAAACCATTTCTTTTATGGGTGTATGACACAGATAATTGTCTTCTTCTGGTGTG  
 GGTGTACAGAGTGTGCGCTGTCTGGCAGTGATGTCTATGACCCGGTATGTGGCTGTCTGCAA  
 35 GCCCTGTACTACTCTACCATCATGACACAACCGGTGTGTCTTGGCTGTCTCTCAGGTCTCT  
 GGGCAGTGGGGCAGTAGTGTCTTAGTAGATACCAGCTTACTTTCCATCTTCCCTACTG  
 GGGACAGAATATAATCAATCACTACTTTTGTGAACCTCCTGCCTCCTGAAGCTGGCTTCC  
 ATAGACACTTACAGCAGAGAAATGGCCATCTTTTCAATGGGCGTGGAATCCTCCTGGCCC  
 CTGTCTCCCTGAITCTTGGTCTTATTGGAATATTATCTCCACTGTATCCAGATGCAGTCT  
 40 GGGGAAGGAGACTCAAGGCTTTTCCACTGTGGCTCCCATCTTATGTGTGTGTCTCTCT  
 CTATGGGTGAGGAATATTCACTACATGCGACCAAACTCCAAGACTACAAAGAACTGGA  
 TAAATGATATCTGTGTTCTATACAGCGGTGACTCCAATGTTGAACCCATAATTATAGC  
 TTGAGGAACAAAGATGTCAAAGGGGCTCTCAGGAAACTAGTTGGAGAAAGTGCTTCTCT  
 CATAGGCAGTGA (SEQ ID NO: 200)

**AOLFR109 sequences:**

MLRNGSIVTEFILVGFQSSSTTRALLFALFLALYSLTAMNGLDIFTSWTDPKLNSPMYFFLG  
 HLSLLDVCFITITPQMLHLVVRDHVSVCCMTQMYVFVCGVAECILLAFMAYDRYVAICY  
 PLNYVPISQKVCVRLVGTAWFFGLINGIFLEYISFREPFRRDNHIESFFCEAPIVIGLSCGDPOFSL  
 50 WAIFADAIVVLSPMVLVTYSVHILATILSKASSSGRGKTFSTCASHLTVVIFLYTSAMFSYMN  
 PHSTHGPKDKPFSLLYITITPMCNPIIYSFRNKEIKEAMVRALGRTRLAQPQSV (SEQ ID NO:  
 201)

ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCTCTGTGGGCTTTCAGCAGAGCTCCA  
 CTTCACACGAGCATGTCTTGTGCCCTCTTCTGGCCCTCTACAGCCTCACCATGGCCATG  
 55 AATGGCCTCATCATCTTTATCACTCTGGACAGCCCAAGCTCAACAGCCCCATGTACT  
 TCTTCTCTGGGCATCTGTCTCTCTGGATGTCTGTCTCATCACACTACCATCCACAGATG



TTGATCCACCTCGTGGTCAGGGACCACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT  
ACTTTGTCTTCTGTGTGGTGTGGCCGAGTGCATCCTCTGGCTTTCATGGCCTATGACCGT  
TATGTTGCTATCTGCTACCCACTTAACATATGCCCCATCAAGCCAGAAGGTCTGTGTCA  
GGCTTGTGGGAAGCTGCCTGGTCTTTTGGGCTGATCAATGGCATCTTCTCGAGTATATTTC  
5 ATTCCGAGGACCCCTTCGCGAGAGACAACCACATAGAAAGCTTCTCTGTGAGGCCCCCAT  
GTGATTGGCCTCTCTGTGGGGACCCCTCAGTTTAGTCTGTGGGCAATCTTTGCCGATGCCA  
TCGTGGTAATTCTCAGCCCATGGTGCTCACTGTCACTTCTATGTGCACATCTCGGCCACC  
ATCCTCAGCAAAAGCCTCCTCCTCAGGTGGGGGAAGACTTCTCTACTTGTGCCTCTCACC  
TGACTGTGGTCATCTTCTCTACACTCAGTATGTTCTCTTACATGAACCCCCACAGACA  
10 CATGGGAGTGCACAAAGACAACCTTCTCCTCTGTACACCATCATACCCCATGTGCA  
ACCCCATCATTTATAGTTTCCGCAACAAGGAAATTAAAGGAGGCCATGGTGAGGGCATTG  
GAAGAACCAGGCTGGCCAGCCACAGTCTGTCTAG (SEQ ID NO: 203)

#### AOLFR110 sequences:

MKIANNVTVEFILLGLTQSQDIQLLVFVLLIFLILPGNFLIIFTRSDPLTAPLYLFLGNLAF  
DASYSFIVPRMLVDFLSEKKVISYRGCTQLFFHLFLLGGGGLLLVVMFAFDRIAICRPLHCST  
VMNPRACYAMMLALWLGGFVHSIQVLLILRLPFCGNQLDNFFCDVRQVILKATGFFVVEL  
LMVFNGLMTLLCFLGLLASYAIVLCHVRRAASEGKNKAMSTCTTRVIIIIMFGPAIFYMCPF  
RALPADKMYSLFHTVIFPLMNPMIYTLRNQEVKTSMKRLLSRHVVQCQVDFIURN (SEQ ID NO:  
20 203)

ATGAAGATAGCAAAACAACACAGTAGTGACAGAAATTAATCCTCCTTGGCTGACTCAGTCTC  
AAGATAITCAGCTCTGGTCTTTGTGCTGATCTTAATTTCTACCTTATCATCTCCCTGGA  
AATTTTTCATTATTTTACCATAAGGTGAGACCTGGGCTCACAGCCCCCTCTATTATT  
25 TCTGGGCAACTTGGCCTTCTGGATGCATCTCACTCTTCAATTTGGTCCAGGATGTTGG  
TGACATCTCTCTGAGAAAAAGGTAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTT  
CTTGCACTTCTCGTGAGGAGGGGAGGATTACTCTGTTGTGATGGCCTTGTACCGCTAC  
ATCGCATCTCGCCGCCCTTGCACTGTTCAACTGTATGAACCTAGAGCCTGCTATGCAA  
TGATTTGTGGCTCTGTGGCTTGGGGTTTTGTCCACTCCATTATCCAGGTGGTCTCATCTC  
30 CGATTGCCCTTTTGTGGCCCAAACCAAGCTGGACAACCTTCTGTGATGTCCGACAGGTCA  
TCAAGCTGGCTTGCACCGACATGTTTGTGGTGAGCTTCTAATGGTCTTCAACAGTGGCCT  
GATGACACTCCTGTGCTTTCTGGGGCTCTGGCTTCTATGCACTGCTCTGCGCATGTTT  
GTAGGGCAGCTTCTGAAGGGAAGAACAAAGGCCATGTCCACGTGCACCACTCGTGTCA  
TTATACTTCTTATGTTTGGACCTGCTATCTTCACTACATGTGCCCTTTCAGGCGCTTACCA  
35 GCTGCAAGATGGTTTCTCTCTTTCACACAGTGATCTTCCATTGATGAATCCTATGATT  
TACCCTTCGCAACAGGAAGTGAAAACCTCCATGAAGAGGTTATTGAGTCGACATGTAGTC  
TGTCAGGTGGATTTTATAATAAGAACTGA (SEQ ID NO: 204)

#### AOLFR111 sequences:

MCYIYLIFKEWTLIFYSLLFLQITPAIMANLTVTEFILMGFSNKNMILHSILFLIYLALM  
GNAVILIMITLDHHLHTPVYFFLNLSFLDLCLISVTAPKSIANSILHNNSISFLGCVSQVFLLS  
ASVLELLTVMSDFRUYAICHPLHYDVMDRSTCVQRTATVSWLYGGLIAMVHTAGTFLSYCG  
SNMVHQQFCDIPQLLAISCSENLIREIALILINVLDFFCFIVIIITYVHVFTVKKIPSTEGSKAY  
SICLPHLLVVLFTSTGFIAYLKPAESPILDAVISVFYTMPLPTFNPIYSLRNKAIKVALGMLIK  
45 KLTCK (SEQ ID NO: 205)

ATGTGTTATATATATTTAATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCT  
TTCTCGACATTACTCTGCAATAATGGCAATCTCACAATCGTGACTGAATTTATCCTTA  
TGGGGTTTCTTACCAATAAAAAATATGTGCATTTTGCAATCGATTCTCTCTGTGTGATTAT  
50 TGTGTGGCTGTGAGGGGAATGTCTCAITATCATGATCACAACATTTGGACCATCATCTCC  
ACACCCCGTGATTTCTCTTGAAGAACTCATCTTCTTGATCTCTGCCTTATTTCAGTC  
ACGGCTCCCAATCTATCGCAATCTTTTGATACACAACAACCTCCATTCACTTGGCTG  
TGTITCCAGGTCTTTTGTGCTTCTTCAAGCATCTGCAGAGCTGCTCCTCCTACCGTGA  
TGTCTTTGACCGCTACTGCTATATGTCAACCTCTGCACTATGATGCATCATGGACAGG  
55 AGCACTGTGTCCAAAGAGCCACTGTGTCTTGGCTGTATGGGGTCTGATTGCTGTGATGC  
ACACAGCTGGCACCTTCTCTTATCTCTACTGTGGGTCCAACTGGTCCATCAGTCTCTCTGT

5 GACATTCCCAGTTATTAGCTATTCTTGCTCAGAAAAATTTAATAAGAGAAATTGCACCTCA  
TCCTTTAATAAGTAGTGTGGATTCTGCTGTTTATGTGCATCATTAACCTATGTCAC  
GCTCTCTCTACAGTCAAGAAGATCCCTTCCACAGAAGGCCAGTCAAAAGCCTACTCTATT  
GCCTTCCACACTTGCTGGTTGTGTTATTTCTTCCACTGGATTCTGCTTATCTGAAGCCA  
GCTTCAGAGTCTCTTCTATTTTGGATGCTGTAATTTCTGTGTTCTACACTATGCTGCCCC  
AACCTTTAATCCATTATATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG  
TTGATAAAGGGAAGCTCACCAAAAAGTAA (SEQ ID NO: 206)

**AOLFR113 sequences:**

10 MKFWHGFSSHLNPMFSSFLLYSLPWINTTIQAWLNLCSLALPVWAMSGAGFLSCCYWHITCSP  
SVVTCSSSQSSDWMQLCTHLCTTSLVFFPSWSGCIQLPLSLRCLIFSVRRKPFLLQDASFRPTSS  
TPWGACECYLLTAMAYDRYLAICRPLHYPIIMTTTLCAKMAAACWCTGFLCPISIVILASQLPF  
CAYNEIQHIFCDPPLLSLACKDTSANILVDFAINAFILITFFIMISYARIIGAVLKIKTASGRKK  
AFSTCASHLAVVLFFGSIFMYVRLKSSYSLTLDRTLAIVYSVLTMPVNPPIYSLRNKEIKAIKR  
15 TIFQKGDKASLAHL (SEQ ID NO: 207)

20 ATGTGTCAACAAATCTTACGGGATTGCATCTCTCTCATACATCATTTGTGCATTAAACAGGA  
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC  
CTTCTCTCTTGTGGGTATCCAGGACTGCAATCTTACATCTTTGGCTGGCTATCTCACTGA  
GTGCCATGTACATCATAGCCCTGTAGGAAACACCATCATCTGACTGCAATCTGGATGGA  
TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTTCTGGCTGCTGTGGACATTGTTA  
TGCCCTCTCGGTGGTACCAAGATGGTAGGACATCTTCTGCTCAGGAGACAGCTCAATCAG  
CITTAGTGCTGTGTTTCACTCAGATGTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG  
CTGCTGCTGACCATGGCTTTTGACCCTATGTAGCCATCTGCAAGCCTCTACAGTACAAGA  
25 GAATTCTCAGCCCTCAAGTGATGCTGGGAATGAGTAGGCAATCACCATCAGACTCATCAT  
AGCCATAACTCCACTGAGTTGGATGGTAGTCACTACCTTTCTGTGGCTCAATGTGTT  
GTCCACTCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGCTGACCCCGTGCCCA  
CGAGCTCTACAGTCTGATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCCTTATTGCT  
GCCTCCTATATCTTAATCTCAAGGCAGTATTGTGCTCTCCTCAAAGACTGCTCAGTTGAA  
30 AGCATTAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGACTATCTAGCTGGGAGT  
GCATCCATCTATGCGGCTGGTTGGGGCAGGATAGTAGCCCTTGACACCCCAAGTCTGCT  
TAGCTGACCTGTACGTGATCATCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC  
CAAACACTCGGGAGAGAATATGGAGTTATCTGATGCATGCTCTTTGACCATTCCAAC  
CTGGGTTCATGA (SEQ ID NO: 208)

35

**AOLFR114 sequences:**

10 MERINHTSSVSEFILLGLSSRPEDQKTLFVLFLIVLVTTITGNLLIILAIRFNPHLQTPMYFSLFSL  
LTDICFTTSVVPKMLMNLSEKKTISYAGCLTQMYFLYALGNSDSCLLAVMAFDYVAVCDPF  
HYVVTMSHHVCLVAVFSCSFPHLHSLHTLLNRLTFCDSNVIHFLCDLSPVLKLSCSISFIN  
40 EIVQMTESPIHLVTRFLCIAFSYIRLLTVLKLIPSTSGRKAFTSCGFYLVTVTLFYGSIFCYVLQP  
PSTYAVKDHAIVTVLSSMLNPFYISLRNKLKQLRLKMSKRS (SEQ ID NO: 209)

45 ATGGAAGAAATCAACCACACAGCAGTGTCTCCGAGTTTATCCTCCTGGGACTCTCTCCC  
GGCCTGAGGACCAAAAGACACTCTTGTCTCTTCTCATCGTGACTGCTGGTACCACATAAC  
AGGGAACCTGCTCATCTCTGGCCATTCGCTTCAACCCCATCTTCAGACCCCTATGATT  
TCTTCTTGAGTTTCTGTCTCTCACTGATATTGTGCTTTACAACAAGCGTTGTCCCAAGATG  
CTGATGCAACTTCTGTGAGAAAAGAAGACCATCTCTATGCTGGGTGCTGTGACACAGATGT  
ATTITCTATGCTTGGGCAACAGTGACAGCTGCCTTCTGGCAGTATGGCCCTTTGACCG  
CTATGTGGCCGTCTGTGACCTTTTCACTATGTACACCACCATGAGCCACCACTGTGTCT  
50 TGCTGGTGGCCTCTCTGCTCATTTTCTCACTCCACTCACTCTGCAACACACTTCTGCTG  
AATCGTCTACCTTCTGTGACTCCAATGTTATCCACACTTTCTGTGACCTCAGCCCTGT  
GCTGAAATTTGCTGCTCTCCATATTGTCAATGAAATTGTGCAGATGACAGAAGACCT  
ATTGTTTGGTGACTCGTTTCTCTGCAATGCTTTCTCTTATATACGAATCTCTACTACCT  
TCTCAAGATTCCTCTCACTTCTGGGAAACGCAAGCCCTTCCACACTGTGGTTTATACCTCA  
55 CCGTGGTGACGCTCTTTATGGAAGCATCTTCTGTGTCTATTACAGGCCCATCCACACTAC  
GCTGTCAAGGACACAGTGGCAACAATTGTTTACACAGTTTGTATCATGCTCAATCTCT

TTATCTACAGCCTGAGAAACAAAGACCTGAACACGAGGCTGAGGAAGCTTATGAGCAAGA  
GATCCTAG (SEQ ID NO: 210)

**AOLFR115 sequences:**

5 MEGFYLRRSHELQMGFKPGRVNQTTVSDFLLLGLSEWPHEQLPLFGIFLGMYLVTMVGNNLLI  
LAISSDPHLHTPMYFLIANLSLTDACFTSASIPKMLANIHTQSIYSYGCLAQLYFLLMFGGLD  
NCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVWCWVLTNCPALMHITLLLTRVAFCAQK  
AIPHFYCDPSALLKLKACSDTHVNELMIITMGLLFLTVPLLLIVFSYVRIFWAVEFVSISSPGGRWKA  
10 FSTCGSHLTVVLLFYGSILMGVYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLNRNDMEKALG  
KLFVSGKTFEL (SEQ ID NO: 211)

ATGGAAGGTTTATCTGCGCAGATCACACGAACTACAAGGGATGGGAAAACACGGCAGA  
GTGAACCAAAACCACTGTTTCAGACTTCTCTCTAGGACTCTCTGAGTGCCAGAGGAGC  
AGCCTCTCTGTTTGGGCACTCTCTTGGCATGTACCTGGTCACCATGGTGGGGAACCTGCTC  
15 ATTATCCTGGCCATCAGCTCTGACCCACACCTCCATCTCCATGTACTTCTTCTGGCCAA  
CCTGCTATTAACGTATGCTGTCTCACTTCTGCCTCCATCCCCAAAATGCTGGCCAACTTC  
ATACCCAGAGTCAGATCATCTCGTATTCTGGGTGCTTGCACAGCTATATTCTCTCTATG  
TTTGGTGCCCTTGACAACTGCTGCTGGCTGTGATGGCATATGACCGCTATGTGGCCATCT  
GCCAACCACTCCATTACAGCACATCTATGAGTCCCAGCTCTGTGCACTAATGCTGGGTGT  
20 GTGCTGGGTGCTAACCAACTGTCTGCCCTGATGGCACACACTGTTGTGACCCGCTGGCT  
TTCTGTGCCAGAAAGCCATCCCTCATTTCTATTGTGATCCTAGTGCTCTCTGAAGCTTGC  
CTGCTCAGATACCCATGTAAACGAGCTGATGATCATCACCATGGGCTTGCTGTCTCTCACT  
GTTCCCGCTCCTGCTGATCGTCTTCTCTATGTCGCAATTTCTGGGCTGTGTTTGTCACTC  
25 ATCTCCTGGAGGGAGATGGAAGGCCCTTCTACCTGTGGTTCTCATCTCACGGTGGTCTG  
CTCTCTTATGGGTCTCTTATGGGTGTGATTACTCTCCATCACTCACTCTACAGAGAG  
GGAAAGTAGGGCTGCTGTCTCTATATGGTGATTAATCCACGCTAAACCCATTCATTAT  
AGCTTGAGGAACAGAGACATGAAGGAGGCTTTGGGTAACATTTTGTCAGTGAAAAACA  
TTCTTTTATGA (SEQ ID NO: 212)

**AOLFR116 sequences:**

30 MDEANHSVVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLTVTSDPRLQSPMYFLLAN  
LSIINLVFCSSATPKMIYDLFRKHKTISFGGCVYQIFFIHAVGGTEMVLLIAMAFDRYVACKPLH  
YLTIMNPORCILFLVISWIIHSVQLAFVVDLLFCGPNELDSFFCDLPRFIKLACIETYTLGFMV  
TANSGFISLASFLILISYIFLVTQKSSGGIFKAFLSMLSAHVIVVVLVFGPLIFFYIFPFTSHLD  
35 KFLAIFDAVITPVLNPVIYTFRNKEMMVAMRRRCSQFVNYSKIF (SEQ ID NO: 213)

ATGGATGAAGCCAATCACTCTGTGGTCTCTGAGTTTGTGTTCTGGGACTCTCTGACTCGC  
GGAAGATCCAGCTCCTCTCTCTCTCTTTTCTCACTGTCTATGATCAAGCTGATAGGGA  
40 AATCTCCTCATGTGTCTAATCTGTGACTCTGACCCCTCGTTTACAGTCCCCCATGTACTTCT  
GCTGGCCAACCTTTCCATCATCAATTGGTATTTTGTCTCCACAGCTCCCAAGATGATTT  
ACTGCTTTTTCAGGAAGCAAGACCACTCTCTTTTGGGGCTGTGTGATTCAGACTCTCTT  
TATCCCTGTGAGTGTGGGGAACTGAGATGGTGTCTGCTCATAGCCATGGCTTTGACCGGAT  
GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCCAAAAGGTGCATTTTGT  
TTTATGATCAATCTCTGGATTATAGGTAATTACTCACTCAGTGATTCAGTTGGCTTTTGTGTA  
45 GACCTGCTGTCTGTGCGCCATAATGAATTAGATAGTTCTTTTGGATCTCTCGGATTTAT  
CAAACTGGCTTGCATAGAGACTACACATTGGGATTCATGGTACTGCAATAGTGGATTT  
ATTCTCTGGCTCTCTTTTAAATCTCATAATCTTCACTTATTTTGGTGATGCTTCAG  
AAAAAATCTTCAGGTGGTATATTCAAGGCTTTCTCTATGCTGTGACGCTCATGTCTTGG  
TGGTTTGTGCTCTTGGGCCATTAACTTTTCTATATTTTCCATTTCCACATCACATCTGT  
50 ATAAATCTCTGCCATCTTTGATGCGAGTATCACTCCCGTTTGAATCCAGCTCATCTACT  
TTTAGAAATAAGAGATGATGGTGGCAATGAGAAGCAGATGCTCTCAGTTTGTGAATTAC  
AGTAAATCTTTTAA (SEQ ID NO: 214)

**AOLFR117 sequences:**

55 MNNTIVFVIKIQIEKSDLYRAISLQEISKISLLFWVLLVISRLLAMTLGNSTEVTEFYLLGFGA  
QHEFWCILFIVELLIVYTSIMGNSGILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSF

BEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDPPYVAICKPLHYTVIMSRVTCIRLVAGSYI  
MGSINASVQTGFTCSLFSCKSNSINHHFCDVPPIALSCSNVDINIMLLVVFVGSNLFTGLVVFIS  
YIYIMATILKMSSSAGRKKSFSFTCASHLTAVTIFYGTLSSYMYLQSHSNNSQENMKVAFIFYGTVI  
PMLNPLIYSLRNKEVKALKVIGKKLF (SEQ ID NO: 215)

5

ATGAATAACACTATTGTATTGTGCATAAAAAACAAATAGAAAAAAGTGACTTGAATATA  
GAGCCATTTCATTGCAAGAAATCTCAAAGATTTCCTTCTTTCTGGGTCCTTCTCTGGTC  
ATTTCTAGACTTTTACTAGCCATGACACTAGGAAACAGCACTGAAGTCACTGAATTCATC  
10 TCTGGGATTGTGGTCCAGCATGAGTTTGGTGATCTCTTCTCATTTGATTCCTCTCATC  
TATGTGACCTCCATAATGGGTAATAGTGGATAATCTTACTCATCAACACAGATCCAGAT  
TTCAAACACTCAGTACTTTTTTCTACAACATTGGGCTTTGTGTATATCTGTACACTTCT  
GCTATCACTCCAAAGATGCTCCAAGCTTCACAGAAGAAAAAGAAATTGATATTTATCCAGG  
GCTGTGTGATACAATCTTAGTTTATGCAACATTTCGAACCACTGACTGTTATCTCTGGCT  
ATGATGGCAGTGGATCCTTATGTTGCCATCTGAAGCCCCCTCACTATACGTGAATCATGT  
15 CCCGAACAGTGCATCCGTTTGGTAGCTGGTGCATACATCATGGCTCAATAAATGCCTC  
TGTACAAACAGGTTTACATGTTCACTGTCTTCTGCAAGTCCAATAGCATCAATCACTTTT  
TCTGTGATGTTCCCTTAATCTTGTCTTCTCATGCTCCAATGTTGACATCAACATCATGTA  
CTTGTTGTCTTGTGGGATCTAACTTGATATTCAGTGGGTGGTGGTCACTTTTCTCATCAT  
CATACATCATGGCCCACTCTGAAAAATGCTTCTAGTGCAGGAAGAAAAATCTCTCTCA  
20 ACATGTGCTTCCCACCTGACCGCAGTCACCAATTTTCTATGGGACACTCTTACATGTAATTT  
GAGCTCTCAITCTAATAATTCAGGAAAAATGAAAGTGGCTTTATATTTTATGGCACA  
GTTATTCCCATTTAAATCCTTTAATCTATAGCTTGAGAAAAAAGGAAGTAAAGAAAGCTT  
TAAAAGTGATAGGGAAAAAGTTATTTTAA (SEQ ID NO: 216)

25 **AOLFR118 sequences:**

MNYHMSASLKJNSNKKQVSEFILLGFGIHSWQHWSLPLALLYLSALAANTLILIIIWQNPSLQQ  
PMYIFLGLCMVDMLGATTIIPKILAIWFDAKVISLPFCFAQIYAIHFVGMESGILLCMAFDRY  
VAICHPLRYPISVTTSSLILKATLFMVLRNGLFVTPVVLAAQRDYCSKNEIHLCSNLGVTSLA  
CDDRPNISQICQLVLAWLGMGSDLSLILSYLILSVLRNSAEAAAKALSTCSSHLTLILFYFTIV  
30 VVSVTHLTEMKATLIPVLLNLVHNIIPPSLNPTVYALQTKELRAAFQKVLFAITKEIRS (SEQ ID  
NO: 217)

ATGAATCATATGCTGCATCTCTCAAAATCTCCAATAGCTCCAATTCAGGCTCTGTGAGTT  
CATCTGCTGGGATTCCCGGGCATTACAGCTGGCAACACTGGCTATCTCTGCCCTGGCA  
35 CTACTGATCTCTCAGCACTTGTGCAAAACACCTCATCTCATCATCATCTGGCAGAACC  
TCTTTACAGCAGCCATGTATATTTCTTGGCATCTCTGTATGTTAGACATGGGCTCTGG  
CCACTACTACTCCCTAAGATCTCGGCCATCTCTGGTTGATGCCAAAGGTTATTAGCCTC  
CTGAGTGCTTTGCTCAGATTTATGCCATTCACTTCTTTGTGGGCGATGGAGTCTGTGATCTC  
TACTGTCATGGCTTTGATAGATATGTGGCTATTTGTCACCCTCTTCGCTATCCATCAATTG  
40 TCACCAGTTCCTTAATCTTAAAGCTACCTGTTCATGGTGCTGAGAATGGCTTATTGTG  
ACTCCAGTGCTGTGCTTGAGCAGCAGCGTGATTATTGCTCCAAGAAATGAAATTGAACACT  
CGCTGTGCTCTAACTTTGGGGTCAACAAGCCTGGCTTGTGATGACAGGAGGCCAAACAGCAT  
TGGCAGTTGGTCTGGCATGGCTTGGAAATGGGGAGTGATCTAAGTCTTATTAATCTGTCA  
TATATTTTGATTCTGTACTCTGTACTGTAGACTGAACCTCAGCTGAAGCTGCAGGCCAAGGCC  
45 TGAGCACTGTAGTTACATCTCAACCCTCATCTCTTTCTTTACACTATTGTTGTAGTGATT  
TCAGTGACTCATCTGACAGAGATGAAGGCTACTTTGATCCAGTCTACTAATAATGTTGTC  
ACAACATCATCCCCCTTCCCTCAACCCTACAGTTTATGCACTTCAGACCAAAAGAACTTAG  
GGCAGCCTTCCAAAAGGTGCTGTTTGCCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:  
218)

50

**AOLFR119 sequences:**

MPLFNSLCWFPTHVTPPSFILNGIPGLRVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHP  
MYFFGHALSLIDLTLCTTLPNALCIFWFSKKEFNACLAQMFFVHGFTGVESGVLMLMALD  
RVIAICPYLRYATLLTPIIAKAEATFLRGVLLMIPFPFLVKRLPFCQSNISHTYCDHMSVVKL  
55 SCASIKVNVYGLMVALLIGVDFDCCISLYTILKAAISLSSSDARQKAFSTCTAHISAIITVYPA

FFTFFAHRFGGHTIPPSLHHIVANLYLLPPTLNPIVYGVKTKQIRKSVIKFFQGDKGAG (SEQ ID NO: 219)

5 ATGCCTCTATTAACTTCATTATGCTGGTTCCAAACAATTCATGTGACTCCTCCATCTTTTAT  
TCTTAATGGAATCCTGGTCTGGAAAGAGTACATGTATGGATCTCCCTCCCACCTGCGACA  
ATGTACATCATCTTCTGTGGGGAATCTTGTTCTTGTTGACCTCATTTATTAAGGAGTCT  
CTTACATCATCCGATGTATTTTTTTTGGCCATGCTCTCTCCCTCAATTGACCTCCTTACCTG  
CACCACCTCATACCAATGCACCTCGCATCTTCTGGTTCAGTCTCAAAGAAATTAACCTTCA  
10 ATGCTTGCTTGGCCAGATGTCTTTGTTTCATGGGTTTCACAGGTGTGAGTCTGGGGTGCT  
CATGCTCATGGCTCTAGACCGCTATATAGCCATTGTACCCCTTTGCGTTATGCTACACAC  
TCACCAACCCATCATTTGCCAAGGCTGAGCTTGCCACCTTCTCGAGGGGTGATTGCTGAT  
GATTCCTTTCCCATCTTGGTTAAGCGTTTGCCTTCTGCCAAAGCAATATTATCTCCCAT  
CGTACTGGCACCACATGTCTGTAGTAAAGCTATCTGTGCCAGCATCAAGGTCACTGTAAAT  
15 CTATGGTCTAATGGTTGCTCTCTGATTGGAGTGTGTGACATTTGTTGTATATCTTTGTCTT  
ACACTTTGATCTCTCAAGGCAGCGATCAGCCTCTCTCATCAGATGCTCGGCAGAAAGGCTT  
CAGCACCTGCACCTGCCATATATCTGCCATCATCATCACTATGTTCCAGCATTTCTCACTT  
TCTTTGCCACCCTTTTGGGGGACACAAATCCCCCTTCTCTCACATCATTTGGGCTAAT  
CTTTATCTTCTTCTCCCAACTCTAAACCTATGTGTTATGGAGTAAAGACAAAACAGAT  
ACGCAAGAGTGTCTATAAAGTTCTTCCAGGGTGATAAGGGTGCAGGTGGA (SEQ ID NO: 220)

**AOLF120 sequences:**

20 MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFLTMYLFTLVENLAHLVVLGDHRLRPMYF  
FLTHSLCEIWTYSVTPVKMLAGFIGVDGKNISYAGLSQLFIITFLGATECFLLAAMAYDRY  
VAICMPLYGYAFVSWGTGTCIRLAAACWLVGFLTPILPIYLLSQLTFCGPNVDHFFSCDAPLLALS  
25 CSDVTPKWTVDVFLVSLAVLLASSMVIASVYGNIVPLVLLHRSAAERKWAFFSTCAHLTVSVSLF  
YGTLEFFMVVQTKVTSSINFKNVSVFYSVVTPEMLNPLIYSLRNKEVKGALGRVFSLNFWKQ  
(SEQ ID NO: 221)

30 ATGCAACCATATACCAAAAACCTGGACCCAGGTAACCTGAAATTTGTCATGATGGGCTTTGCTG  
GCATCCATGAAGCACACCTCCTCTTCTCATACTCTCTCACATGCTACCTGTACCTGTACCTGT  
GTGGAGAATTTGGCCATCATTTTAAAGTGGTGGGTTTGGACCAACCGACTACGGAGACCCATGT  
ATTTCTTCTGACACACTTGTCTGCTTGAAATCTGCTACACTTCTGTTACAGTGCCCAAG  
ATGCTGGCTGGTTTATTTGGGGTGGATGGTGGCAAGAATATCTCTATGCTGGTGGCTAT  
35 CCCAGCTCTTCATCTTACCTTTCTTGGGGCAACTGAGTGTTCCTACTGGCTGCCATGGCC  
TATGATCGTTATGTGGCCATTTGTATGCTCTCCCAATGAGGGGCTTTGTGTCTGGGGCAC  
CTGCATCCGCTCTGGCAGCTGCTGTTGGCTGGTAGGTTTCTCACACCATCTTGCCAATCT  
ACCTCTTGTCTCAACATATTTTGTGGCCAAATGTCATTGACCATTTCTCTGTGATGCC  
TCACCTTGCTAGCTTGTGCTGCTCAGATGTCACCTTGGAAAGGAGACTGTGGAATTTCTCG  
40 TGCTCTGGCTGTGCTACTGGCTCTCTATGGTCAATGCTGTGTCTATGGCAACATGCTC  
TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCCTTCTCACTGTGCGAG  
CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTCTTTATGTATGTCCAGACCAAG  
GTGAGCTCCTCCATCAACTTCAACAAGGTGGTATCTGCTCTCTACTCTGTTGTACAGGCCAT  
GCTCAATCCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGAGCTCTGGGTGAGTCT  
TTTCTCTCAACTTTTGGAAAGGACATGA (SEQ ID NO: 222)

**AOLF121 sequences:**

45 MKRKNFTEVSEFIIFLGSSFGKHQITLVFVFLTVYILTLVANIHVTIICDHHLHTPMYFFLSMLA  
SSETVYTLVIVPRMLLSLFIHNPISLAGCATQMFFVILATNNCFLLTAMGYDRYVAICRPLRY  
50 NYGMSKGLCAQLVCGSFGIGLTMAVLHVLTAMFNLPGFTVVDHFFCDIYPMKLSCIDTITNEII  
NYGVSSVFIYVPIGLIFISYVLVISSILQIASAEGRKKTATCTVSHLTVVIVHCGCASIALYKPKSES  
SIEKDLVLSVTVTIITPLNPNVYSLRNKEVKDALCRVVGGRNIS (SEQ ID NO: 223)

55 ATGAAGAGAAAGAACTTCACAGAAGTGTGAGAATTCATTTTCTTGGGATTTTCTAGCTTTG  
GAAAGCATCAGATAACCCCTCTTTGTGGTTTCTCAACTGTCTACATTTTAACTCTGGTGTGCT  
AACATCATCATTTGTGACTATCATCTGCAITGACCATCATCTCCACACTCCGACATGATTTCTT  
CCTACAGTGTGCTAGTTCAGAGACGGTGTACACACTGGTCAATGTGCCAGAAATGCTT

TTGAGCCTCATTTTTTCATAACCAACCTATCTCCTTGGCAGGCTGTGCTACACAAATGTTCTT  
TTTTTTATCTTGGCCACTAATAATGTCTCTCTGCTTACTGCAATGGGGATGACCCGTATG  
TGCCCATCTGCAGACCCCTGAGATACACTGTCACTGATGACGAAGGGACTATGTGCCAGCT  
GGTGTGTGGGTCTCTTGGCATTGGCTTGACTATGGCAGTTTCTCCATTGTGACAGCCATGTTT  
5 AATTITGGCGTTCTGTGGCAGAGTGGTAGACCACTTCTTTGTGACATTACCCAGTCATGA  
AACTTTCTTGCAATTGATACCACTATCAATGAGATAATAAATTATGGTGTAAAGTTCATTGT  
GATTTTTGTGGCCATAGGCCGTGATATTTATCTCCTATGTCCCTGTGATCTTCTCCATCCCTT  
AAATGGCCTCAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGTCTCCCACTCACTGT  
GGTATTGTCCACTGTGGCTGTGCCTCCATTGCCTACCTCAAGCCGAAGTCAGAAAGTTCA  
10 ATAGAAAAAGACCTTGTGTCTCAGTGACGTACACCATCATCACTCCCTTGTCTGAACCTGA  
TTGTTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGACAGATTGTGGGCAGAA  
ATATTTCTTAA (SEQ ID NO: 224)

# **AOLFR122 sequences:**

15 MEWENQTLVVEFFLGHSHVPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL  
SFLDICVTTTSPISLTVSFLSERKTISFSGCAVQMFLGLAMGTTTCVLLGMMAFDRYVAICNPLR  
YPIIMSKNAYVPMVAGSWFAGIVNSAVQTTFVQLPFCRKNVINHFSECHLAVMKLACADISGN  
EFLMLVATILFTLMPLLLVISYSLIISLKIHSSEGRSKAFSTCSAHLTVVIIIFYMTGLFMKPKKS  
KETLNSDDLDATDKIISMFYGVMTMPMNPPLIYSLRNKDVKEAVKHLPNRRFFSK (SEQ ID NO:  
20 225)

ATGGAATGGGAAACCAAACCATTTCTGGTGGAAATTTTTCTGAAGGGACATTCTGTTCACC  
CAAGGCTTGAGTTACTCTTTTTGTGCTAATCTCATAATGATGTGGTCATCTCTCTGGGG  
25 AATGGTACTCTCATITTAATCAGCATCTTGGACCCCTCACCCCTATGTACTTCTT  
TCTGGGAAACCTCTCTCTTGGACATCTGCTACACCACCACTCTATTCCCTCCACACTAG  
TGAGCTTCTCTTCAGAAAGAAAGACCATTTCTCTTCTGGCTGTGACAGTGCAGATGTCTCTT  
GGCTTGGCCATGGGGAACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTACGCGCTATG  
TGGCTATCTGCAACCCCTCTGAGATATCCCATCATCATGAGCAAGAATGCCATGTATACCCAT  
GGCTGTGTGGGTCTGGTTTGACAGGATGTGCAACTCTGCAAGTACAAACTACATTTGTAGTA  
30 CAATGGCTTCTCTGAGGAAGAATGTCAATCAATTTCTCATGTGAAATTTCTAGCTGTCAT  
GAAGTTGGCCTGTGCTGACATCTCAGGCAATGAGTTCTCATGCTTGTGGCCACAATATGT  
TTCACATTTGATGCCACTGCTCTTGATAGTTATCTCTTAATCAATTAATCATTTCCAGCATCT  
CAAGATTCACTCTCTGAGGGGAGAAGCAAAGCTTTCTCTACCTGCTCAAGCCCATCTGACT  
GTGGTCATAAATTTATATGAGGACCATCTCTTCAATGTATATGAAGCCCAAGTCTCAAGAGA  
35 CACTTAATTCAGATGACTTGGATGCTACCGACAAAAATATATCCATGTTCTATGGGGTGAT  
GACTCCCATGATGAATCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGAAGAGGCAGT  
AAAACACCTACCGAACAGAAGTTCTTAGCAAGTGA (SEQ ID NO: 226)

# **AOLFR123 sequences:**

40 MYRFTDFDVSNISIVLNHVLYFTTQQAGDLEHMETRNSAMTEFFLVGLSQYPELQLFLFLCL  
IMYMILLGNSLLIITILDSRLHTPMYFFLGNSFLDICYTSSSIPPLMIIFMSERKSISIFGALQM  
VVSLLGSTETCVLLAVMAYDHYVAICNPLRYSIIMNGVLVYQMAAWSWIIGCLTSLLTQVL  
MMLPCFGNNVDHITCEILLKLKLVCSDTITNVLIMTVTNIVSLVILLLLIFISYVFLSSILRINCAE  
GRKKAESTCSAHSIVVLFYQSALFMYMKPKSKNTNTSDEIIGLSYGVVSPMLNPIIYSLRNKEV  
45 KEAVKKVLSRHLHLKLM (SEQ ID NO: 227)

ATGTACAGATTACAGATTTGATGTATCAACATTTCAATTTACTGAAATCATGTCTTTT  
CTATACTACCCAGCAGGCAAGTGACCTAGAACACATGGAGACAAGAAATTAATCTGCCCAT  
GACTGAATCTTTCTGGTGGGGCTTTCCTCAATATCCAGAGCTCCAGCTTTTCTGTCTCTGCT  
50 TCTGCTCATCATCATGATATAATCTCTGGGAAATAGCCTCTCATTAATCATCAACCAT  
TTGGATTCTCGCCTCCATCTCCATGTATTTCTTCTTGGAAACCTCTCAATCTTGGACAT  
CTGTTACACATCTCATCTCCATCTCTCAATGCTTATTAATTTATGTCTGAGAGAAAAATCA  
TCTCTTCTATGGCTGTGCTCTGCAATGGTGTGTCCTTGGCTTGGGCTCCACTGAGTGT  
GTCTCTCTGGCTGTGATGGCCTATGACCACTATGTGGCCATCTGCAACCCCATCTGAGTGT  
55 CCATCATCATGAACGGAGTGTGTATGTGCAAAATGGCTGCAATGGTCTGGATCATAGGCTG  
TCTGACCTCCCTATTGCAACAGTTCTGACAATGATGTGGCTTTCTGTGGGAATAATGTC

- ATTGATCATATTACCTGTGAAATTTTGGCCCTTCTAAAACCTGTTTGTTCAGATATCACCAT  
CAATGTGCTTATCATGACAGTGACAAATATGTTTCACTGGTGATTCCTCTACTGTTAAATT  
TCATCTCTCATGTGTTTATTTCTCTCTCCATCCTGAGAATAATTTGTGCTGAGGGAAGAAAG  
AAAGCCTTCTCTACCTGTTGAGCGCACTCGATTGTGGTCATCTTATCTACGGTTCAGCCCT  
TTTTATGTACATGAAACCCAAAGTCAAAGAACACTAATACATCTGTAGAGATTATTGGGCTG  
TCTTATGGAGTGGTAAGCCCAATGTTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG  
TCAAAGAGGCTGTAAGAAAGTCTGTAGCAGACATCTGCATTATTGAAATGTGA (SEQ  
ID NO: 228)
- 10 **AOLFRI24 sequences:**  
MNH5VVFTEFILGLTKKPELQGIIFLFLIVYLVAFLGNMLJIAKIYNNLTHTPMYVFLLTAVV  
DICTTSHPKMLGTMLTSENTISYAGCMSQLFLFTWSLGAEMVLFITMAYDRYVAICFPLHYST  
VMNHMCMVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPLLALSCSPVRINEV  
MVYVADITLAIGDFILTCSYGFIIIVAILRIRTVGKRAKAFSTCSSHLTUVVTLYYSPVIYTYIRPASS  
YTFERDKVVAALYLTVPITLNPVVSFQNMREQAIRKVFAFLKH (SEQ ID NO: 229)
- 20  
ATGAATCAGCGTGTGAACCTGAGTTCATTATTCTGGGCTCACCAGGCTGAACTCC  
AGGGAATATCTTCTCTTTTCTCATTTGCTATCTTGTGGCTTTTCTCGGCAACATGCTC  
ATCATCTGATGCCAAATCTATAACAACACCTTGATACGCGGATGATGTTTCTCTCTGAC  
ACTGGCTGTTGTGGACATCATCTGCACAACAGCATCATCCGAAGATGCTGGGGACAT  
GCTAACATCAGAAATACCATTTTATATGACAGGCTGCATGTCCAGCTCTTCTTGTTCACA  
TGGTCTCTGGGAGCTGAGATGGTCTCTTACCACCATGGCTATGACCGCTATGTGGCCA  
TTTGTCTTCCCTCTTCTTACAGTACTGTTATGAACCACCATATGTGTGAGCCTTGCTCAGC  
ATGGTTCATGGCTATTGACAGTACCAATTCTGGGTGCACACAGCTCTTATCATGAGGTGTA  
CTTCTGTGGGCCAAACACCATGACCACTTCTCTGTGAGATACCCCCAATGCTGGCTTGT  
25 TCGTGTAGCCCTGTGAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCTGGGCCA  
TAGGGACTTTATCTTACCTGCACTCTCTATGGTTTATCATTTGTGCTATTCTCCGATC  
CGCACAGTAGAAGGCAAGAGGAAGGCCCTCTCAACATGCTCATCTCATCTCACAGTGGTG  
ACCCTTTACTATTCTCTGTAATCTACACCTATATCCGCCCTGCTTCCAGCTATACATTGA  
AAGAGACAAGGTGGTAGCTGCACCTTACTCTTGTGACTCCCAATTAACCCCGATGGTG  
30 TACAGCTTCCAGAATAGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTTCTGAAA  
CACTAG (SEQ ID NO: 230)
- AOLFRI25 sequences:**  
35 MTNQTMMEFLVRFTEWVLLRLHALLFSLIYLTAVLMNLVILLMILDHRLHMAAMYFFLRH  
LSFLDCLISATVPKSIILNSVASTDSIFLGCVLQFLVLVLLAGSEIGLTAMSYDRYAAICPLHC  
EAVMSRGLCVQLMALSWLNRGALGLLYTAGTFSLNFYGSDELHQFFCDVPALLKLTCSKEHAI  
ISVSVAIGVCYAFSLCVIVSVYVYFSAVLRISQRQKAFSNVCVPHLIVTVFLVTGAVAYL  
KPGSDAPSIDLLVSVFYSVAPPTLNPVYICLNKNDIKSLSKVLVWNRSSGVMKDD (SEQ ID  
40 NO: 231)
- ATGACCAATCAGACACAGATGATGGAATTTCTTGCTTGTGAGATTTACTGAGAATTGGGTGC  
TCTGAGGCTGCATGCTTTGCTCTTCTCACTGATCACTACCGCTGTGCTGATGAATTTA  
GTATCATTTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTTCTCTCG  
45 ACATTTGCTCTTTAGACCTGTGTCTCATTTCTGCCACAGTCCCAAATCCATCTCAACT  
CTGTGCGCTCCACTGACTCCATCTCTTCTGGGTGTGTGTGTGAGCTCTTCTTGTGTGTA  
CTGTGCTGGATCAGAGATTGGCATCTCTACTGCCATGTCTATGACCGTATGCTGCCA  
TCTGCTGCCCCCTACACTGTGAGGCTGTGATGAGCAGAGGGCTCTGTGTCCAGTTGATGGC  
TCTGTCTGGCTCAACAGAGGGGCTTGGGACTCTGTACACAGCTGGAACATTTCTCTCTG  
AATTTTATGGCTCTGTAGCTACATCAGTCTTCTGCGATGTCCTGCGCTCCCTACTAAAGCT  
50 CACTGTGTTCTAAAGAACATGCCATCATTAGTGTGAGTGTGGCCATTGGGGTCTGTTATGCA  
TTTTCTGTTTATGTTTGCATTGTAGTTTCTATGTGTACATTTTCTCTGTGTGTTAAGGAT  
ATCAGAGAGCAGAGACAATCCAAAGCCCTTTTCAACTGTGTGCTGCTCACTCATCTTGTCT  
ACTGTGTTCTTGTAAACAGGTGCTGTTGCTATTTTAAAGCAGGGTCTGATGACCTTCTAT  
55 TCTAGACTTGTGTTGCTGTGTTCTATTCTGTGCACTTCAACCTTGAACCTGTTATCT

ACTGTCTGAAGAACAAGGACATTAAATCCGCTCTGAGTAAAGTCTGTGGAATGTTAGAA  
CGAGTGGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

**AOLFR126 sequences:**

- 5 MFYLFCFIFORTCSEEMEBEENATLLTEFVLTFGLHQPDCKIPLFLAFLVIYLITMGNLGLVLIV  
KDPHLHPMYLFLGSLAFVDSLSSTVTPKMLINFLAKSMISLSECMVQFSLVTTVTTECELL  
ATMAYDRYVAICKALLYPVMITNELCQLLVLSFIFGLLHALIHEAFSRLTFCNSNIQHIFYCDII  
PLLKISCTDSSINFLVMFIFAGSVQVFTIGTILISYTHILFILEKKSIRKAVSTCGAHLISVSLY  
YGPLTFKYLGSASPQADDQDMMESLFTYVIVPLNPMIYSLRNKQVIAFSTKMFKSNV (SEQ ID  
10 NO: 233)

- ATGTTCCCTTTACCTTTGCTTCATTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA  
ATGCAACATTGCTGACAGAGTTTGTCTCACAGGATTTTACATCAACCTGACTGTAAAT  
ACCGCTCTTCTGGCATTCTGGTAAATATATCTCATCACCATCATGGGGAATCTTGGTCTAA  
15 TTGTTCTCATCTGGAAGAGCCCTCACCTTCATATCCCAATGTACTATTCTCTGGGAGTTTA  
GCTCTTGTGGATGCTCTTGTATATCATCCACAGTGACTCCGAAGATGCTGATCAACTTCTTAG  
CTAAGAGTAAGATGATATCTCTCTGTAATGCATGGTACAATTTTTTCCCTTGTAAACCACT  
GTAACACAGAATGTTTCTCTTGGCAACAATGGCATATGATCGCTATGTAGCCATTGGCA  
AAGCTTTAGCTTTATCCAGTCATTATGACCAATGAACTATGCATTGAGCTATTAGTCTTGTCA  
20 TTTATAGGTGGCTCTTTCATGCTTAAATCCATGAAGCTTTTTCATTAGATTAACCTCTG  
TAATTCACACATAATACAACACTTTTACTGTGACATTATCCCATTTGTTAAAGATTTCCTGTG  
CTGATTCTCTTAACTTTCTAATGGTTTATTTTCTCGCAGGTTCTGTTCAAGTTTATACCA  
TTTGGAACTATTCTTATATCTTATACAAATATCTCTTACAACTTAGAAAAAGAAGTCTATC  
AAAGGGATACGAAAAGCTGTCTCCACCTGTGGGGCTCATCTCTTATCTGTATCTTTATACT  
25 ATGGCCCCCTCACCTTCAAATATCTGGGCTCTGCACTCCGACAGATGAACCAAGATAT  
GATGGAGTCTCTATTTTACACTGTCTAGTTCTTTATTAATCCCATGATCTACAGCTGA  
GAAACAAGCAAGTAATAGCTTCATTCAAAAAATGTTCAAAGCAATGTTTAG (SEQ ID  
NO: 234)

**AOLFR127 sequences:**

- 30 MSNEDMEQDNTLLTEFVLTLGLTYQPEWKMPFLVFLVIYLITVWNLGLIALIWNDPQLHIPM  
YFGLGSLAFVDAWISSVTPKMLVNFILAKNRMISLSECMQIFFSFAFGGTTCECFLLATMAYDRY  
VAICKPLLYPVMNNSLCIRLLAFSFLGGFLHALIHEVLIFRLTFCNSNIHIFYCDIPLFMISCTD  
PSNLFMVLFSISQIVTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHLISVSLYYGPLIF  
35 MYLRPASFPQADDQDMIDSVFYTHIPLNPIYSLRNKQVIDSFTKMYKRVN (SEQ ID NO: 235)

- ATGTCGAATGAGGACATGGAAACAGGATAATACAACATTGCTGACAGAGTTTGTCTCACA  
GGACTTACATATGACCAGAGTGGAATAATGCCCTGTCTTGGTGTCTCTGGTGATCATATC  
40 TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTCTTATCTGGAATGACCCACAACCTCAC  
ATGCCCATGTACTTTTTCTGGGAGTTTAGCCTTTGTGTGCTGGATATCTTCCACAGT  
AACTCCCAAAATGTGGTTAATTTCTTGGCCAAAAACAGGAATGATATCTGTCTGAATGC  
ATGATTCAAATTTTTCTTGTGCAITTTGGTGGAACTACAGAATGTTTCTCTTGGCAACAAT  
GGCATATGATCGCTATGTAGCCATATGCAAACTTTACTATATCCAGTGATTATGAACAAT  
45 TCATATGTCATACGGCTGTGTAGCCTTCTCATTTTTAGTGGCTTCTCCATGCCTTAATCA  
TGAAGTCTTATATTCAGAITAACCTTCTGCAATTCTAACATAATACATCAATTTTACTGTG  
ATATTATACCAGCTGTTATGATTTCTCTGTACTGACCCTTCTAATAATTTCTAATGGTTTGA  
TTTTGTCTGGCTCAATTCAGGTAATCACCATTGTGACAGTCTCTAATTTCTACACATTTGCT  
CTTTTCACAAATCTAAAAAAGAAGTCTGTGTAGAGGCGTAAGGAAAGCCCTTTTCCACCTGTG  
GAGCCCATCTCTTATCTGTCTCTTATATATATGGGCCCACTATCTCTCATGTATTGGCCCTT  
50 GCATCTCCACAGCAGATGACCAAGATGATGATAGACTCTGTCTTTATACAAATCATATTC  
CTTTGTCTAAATCCCATATATCAAGTCTGAGAAATAACAAGTAATAGATTCAATTCACAAA  
AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

**AOLFR128 sequences:**

- 55 METQNLTVVTEFILLGLTQSQDAQLLVFLVIFYLIILPGNFIIFTIKSDPGLTAPLYFFLGNLA  
LLDASYSFIVPRMLVDFLSEKKVISYRSCITQLFFHLFGAGEMFLLVMAFDRIYAIACRPLHY



STIMPRACYALS LVLVWLGFFIHSIVQVALIHLHPFCGPNQLDNFFCDVPQVIKLACTNTFVVVEL  
LMVNSGSLLSLCLFGLLASAYAVILCRIREHSSEKSKAISTCTTHIIIFLMFGPAIFYITPCFQAFF  
ADKVVSLFHTVIFPLMNPVIYITLRNQEVKASMRKLLSQHMF (SEQ ID NO: 237)

- 5 ATGGAACACAGAACTCACAGTGGTGACAGAAATTCATTCTTCTGGTCTGACCCAGTCTC  
AAGATGCTCAACTTCTGGTCTTGTGCTAGTCTTAATTTTCTACCTTATCATCTCTCCCTGGGA  
AATTTCTCATCATTTTCTACCATAAAGTCAGACCCCTGGGCTCACAGCCCCCTCTATTTCTT  
CTGGGCAACTTGCCCTTACTGGATGCATCTACTCCTTCAATTTGGTGTCCAGGATGTTG  
GTGGAATCTCCTCTCTGAGAAGAAGGTAATCTCCTATAGAAGCTGCATCACTACGCTCTTTT  
10 TCTTGCAATTTTCTGGAGCGGGAGAGATGTTCTCCTCGTTGATGGCCTTGACCGCTAC  
ATCGCCATCTGCCCGGCTTACACTATTCAACCATCATGAACCCTAGAGCCTTGCTATGCAT  
TATCGTTGGTCTTCTGGCTTGGGGCTTATCCATTCCATTGTACAAGTAGCCCTTATCTG  
CACTTGCCTTTCTGTGGCCAAACCAGCTCGATAACTTCTTCTGTGATGTTCCACAGGTCAT  
CAAGCTGGCCCTGACCAATACCTTTGTGGTGGAGCTTCTGTAGTGTCTCCAACAGTGGCCGT  
15 CTGAGCTCCCTGCTGCTTCTTCTGGGCTTCTGGCTCTATGCACTGCATCTCTGTGATAAG  
GGAGCACTCCTCTGAAGGAAAGAGCAAGGCTATTTCACATGCAACCCACCATATTATCAT  
ATAATTCTCATGTTTGGACCTGCTATTTCATCTACACTTGGCCCTTCCAGGCTTCCAGC  
TGACAAGGTAGTTTCTTTTCCATACTGTCATCTTTCCTTGTATGAACCTGTTATTTATA  
CGCTTGCACCAAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTTG  
20 CTGA (SEQ ID NO: 238)

**AOLFR129 sequences:**

- MALYFSLILHMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLGLTSSQDVEFLFLALFSVI  
YVVTVLGNLLIVTVFNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT  
25 QIFLLHLLGGVEMVLLVSMADFVYVYICKPLHYMTIMNKKVCVLLVTVSWLLGLLHSGFQIPF  
AVNLPFCGPNVVDISFCDPLVTKLACIDIYFVQVIVANSGLISLFCFILLISYSLILITKIHNSPT  
GQSKARSLTAAHTIYVLFPGCFIHYTWPFNGHNSVDKFLAVFYTIITPILNPIIYTLRNKEMKISMK  
KLWRAFNVSREDT (SEQ ID NO: 239)
- 30 ATGGCTCTTTATTTTCACTCATACTCCATGGTATGAGTGATCTTTTCTTCTCTACAGG  
TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAACTATTAATCAATCTCAAGTGTC  
AGAATTCATTTTGTCTGGAGCTGACCACTGCCAGGATGTAGAGTTTCTTCTCTTGGCCCTCT  
TCTCGGTATCTATGTGGTACACAGTTTGGGTAACTCTTAATTATAGTCACAGTGTTTAAAC  
ACCCCTAACCTGAATACTCCCATGTATTTCTCCTTGGTAATCTCTCTTTGTAGATATGAC  
35 CTTGCTTCTTTTGGCAACCCCTAAGGTGATTCTGAACCTGTTAAAAAGCAGAAGGTAATT  
TCTTTTGTCTGGGTGCTTCACTCAGATATTCTCCTTCACTTACTGGGTGGGGTGAAGATGGT  
ACTGTGGTCTCCATGGCTTTTGACAGATATGTGGCCATTTGTAAAGCCCTACACTACATG  
ACCATCATGAACAAGAAGGTATGTGTTTGTCTGTAGTGAACCTCATGGCTCTTGGGTCTCC  
TTCACAGGGTCTTCAGATACCATTTGCTGTGAACCTTGCCCTTTGTGGTCCCAATGTGGTA  
40 GACAGCATTTTGTGACCTCCCTTTGGTTACTAAGCTTGCTCTGTATAGACATATATTGTT  
ACAGGTAGTCATTTGTGCCAACAGTGGCATAATCTCCCTGAGCTGTTTCATTATTTTGCTT  
TCTCTACAGCTGTGATCTCCTACATAACCATTAAGAACCACCTCTCCTACTGGGCAATCTAAAGC  
CCGTTCACATTTGACTGCTCACATCACAGTGGTGATTCTCTTCTTGGGCCATGCATCTTTA  
TCTACATTTGGCCCTTCGGCAACCACTCTGTAGATAAGTTCCTGCTGTGTTTGTATACCATC  
45 ATCACTCCTATCTTGAATCCAATTATCTATCTCTGAGAAACAAAGAAATGAAGATATCCA  
TGAAAAAACTCTGGAGAGCTTTTGTGAATCTAGAGAAGATACCTTAG (SEQ ID NO: 240)

**AOLFR131 sequences:**

- MASTSNVELTIFGLQDPVAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS  
LVESYSSTIAKPIIDLLAKIKTISLEGCLTQIFFHHFGVAEILLIVMAYDCYVYICKPLHYMNI  
50 ITRQLCHLLVAGSWLGGFCHSIQILVJQLPFCGPNVDIHYFCDLQPLFLCLACTDIFMEGVIVLA  
NSGLFSVSFLLVSSYIVLVNLRNHSAGEHRHKLSTCASHITVILFPGPAIFYLMPRSTHED  
KLAVAFYTVITPMLNPIIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)
- 55 ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTTCACTGGCCTTTTCCAGGATCCAGCTG  
TGCAGAGTGTATGCTTTGTGGTGTCTCCCGGTGTACCTTGCCACGGTGGTGGGCAATGG

CCTCATCGTTCTGACGGTCAAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTTCTCCTTA  
 GCTGCTGCTCTTGGTGGAGATCAGTTATTCCTCCACTATCGCCCTAAATCATCATAGAC  
 TTAATTGCGCAAGATTAACCAATCTCTCTGGAAGGCTGTCTGACTCAGATATTTCTTCTCCA  
 CTCTCTTTGGGGTGTCTGAGATCCTTTTGATTGTGGTGATGGGCTATGATTGCTACGTGGCC  
 5 ATTTGCAAGCCTTCTCATTTATGAACATTATCAGTCGTCAACTGTGTCATCTTGGTGGC  
 TGGTTCTCGGCTGGGGGGCTTTGTGCACTCCATAATTCAGATTCTCGTTATCATCCAAATTGC  
 CCTTCTGTGGTCCCAATTGTGATTGACCACATTTCTGTGACCTCCAGCCTTTATTCGAAGCT  
 GGCTGCATGACACCTTCATGGAGGGGGTTATTGTGTGGCCAAACAGTGGATTATTCTCTG  
 TCTTCTCTCTCATCTTGGTGTCTCTTATATTGTCACTTGTGTCACCTTGAGGAACCAT  
 10 TCTGCAGAGGGGAGGCACAAAGCCCTCTCCACTGTGCTTCTCACATCAGAGTGGCCATCT  
 TGTTTTTTGGACGCTGCTATCTTCTCTACATGCGACCTTCTTCCACTTTCAGTGAAGATAAA  
 CTGTGGGCTGTAATCTACACGGTCAACCCCATGCTGAACCCCATCATTTACACACTCAG  
 GAATGCAGAGGTGAAAATGCCATAAGAAGATTGTGGAGCAAAAAGGAGAAATCCAGGGA  
 GGGAGTGA (SEQ ID NO: 242)

**AOLFR132 sequences:**

MVATNNVTEHIFVGSQNWSEQRVISVMFLMYTAVVLGNGLIVVTILASKVLTSPMYFFLSYL  
 SFVEICYCSVMAPKLIFFSFIKRVISLKGCLTQMFLSHFFGGTEAFLMMVAYDRYVAICKPL  
 HYMAIMNQRMCGLLVRIAAGGGGLHSVGTFLIFQLPCFGPNIMHDYFCDVHPVLELACADT  
 20 FFISLLIITNGSSISVSPFVLMASYLIJLHFLRSHNLEGGHKLSTCASHVTVVDLFFIPCSLVYIR  
 PCVTLPADKIVAVFYTVVTPLLNPVYSFRNAEVENAMRRFIFGGKVI (SEQ ID NO: 243)

ATGGTTGCTACAAACAATGTGACTGAAATAATTTTCGTGGGATTTTCCAGAATTGGAGTG  
 AGCAGAGGGTCAATTTCTGTGATGTTTCTCTCATGTACACAGCTGTTGTGCTGGGCAATGG  
 25 CTTCAATTTGGTGACCATCTGGCCAGCAAGAGTGTCTACCTCCCCCATGTATTTCTTCTCA  
 GCTACTTATCCTTTGTGGAGATCTGCTACTGTTCTGTGATGGCCCCCAAGCTTATCTTTCAG  
 TCCITTTATCAAGAAGTCAATTTCTTCAAGGGCTGCTCACAGAGATGTTTCTCTCC  
 ATTTCTTGTGGTGGCACTGAGGCCTTTCTCTGTGATGGTGTATGGCCATGACCGCTATGTGGC  
 CATCTGCAAGCCCTTGCATACATGGCCATCATGAACAGCGAATGTGTGCTCTCTCGTG  
 30 AGGATAGCATGGGGGGGGGGCCTGCTGCAATTCGTGTGGGCCAAACCTTCTGATTTTCCAGC  
 TCCCGTCTGTGGGCCCAACATCATGGACCACTACTTCTGTGATGTCCACCCAGTGCTGGA  
 GCTGGCTGGCGAGACACCTTCTTCATTAGCCCTGCTGATCATACCAATGGCGGCTCCATC  
 TCCGTAAGTCAGTTTCTCTGTGCTGATGGCTTCTACCTGATCATCTGCACTTCTGTGAGAAG  
 CCACAACCTGTAGGGGGGAGCAGCAAGGCCCTCTCCACTGTGCTCTCATGTGACAGTTGTG  
 35 GACCTGTTCTTCATACCTTGCTCCTTGGTCTATATTAGGCCCTGTGTACCCCTCCCTGCAAG  
 CAAGATAGTTGCTGATTTTATACAGTGGTCACACCTCTCTTAAACCCTGTGATTTACTCCT  
 TCAGGAATGCTGAAGTGAAAAATGCCATGAGGAGATTATTGGGGGAAAAAGTAATTTGA  
 (SEQ ID NO: 244)

**AOLFR133 sequences:**

MTEFIELVLSPNQEVQRVCFVIFLYTAIVLGNFLIVLTVMTSRLGSPMYFFLSYLSFMEICYS  
 SATPKLISDLLAERKVISWVGMAQLFFLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN  
 WQVCTVLVGLAVWVGFMHSAQILLIFHLLFCGPNVINHYFCDLVLPLKLACDSCTFLGLIVAN  
 40 GGTLSYISVFGVLLASVMVILLHLRTWSSEGWCKALSTCGSHFAVILFKGFCVNSLRSLPTLPI  
 DKMVAVFYTVITAILNPVYISLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

ATGACTGAATTCATTTTCTGGTACTTCTCCCAACCAAGGAGTGCAGAGGGTTGCTTTG  
 TGATATTTCTGTCTTGTACACAGCAATGTGCTGGGGAATTTCTCTATTGTGCTCACTGTC  
 ATGACCACAGAGAAGCCTTGGTTCCTCCCATGTACTTCTCTCAGCTACCTCTCTCATGGA  
 50 GATCTGCTACTTCTCCGCTACAGCCCCCAACCTCATCTCAGATCTGCTGGCTGAAAGGAAA  
 GTCATATCTTGGTGGGGCTGATGGCACAGCTTTTCTTCTGCACTCTTTGGTGGCACTGA  
 GATTTTCTGCTCACTGTGATGGCCATGACCACTATGGGCCATCTGCAAGCCCTCAGC  
 TACACCCATCATGAACCTGGCAGGTGTGTACTGCTCTGTAGGAATAGCATGGGTGGGA  
 GGCCTCATGCAATCTCTTGACAAATCTTCTCATCTTCCACCTGCTTCTGTGGCCCAA  
 55 TGTGATCAATCACTATTCTGTGACCTAGTTCCTCTTCTCAAACCTTGCTGTCTGACACCT  
 TCTCATTTGGTCTGCTGATTTGTGCCAATGGAGGCCCTGTCTGTGATCAGTTTGGGGT

CCTCTTAGCATCCTATATGGTCATCTTGCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG  
TGCAAAGCCCTCCACCTGTGGGTCCCATTCGCTGTGGTTATCTTGTTCTTTGGGCCGTG  
CGTCTTCAACTCTCTGAGGCCCTTACCACCTGTGCCATAGACAAGATGGTGGCTGTGTTCT  
ACACAGTGATAACCGCGATCTGAACCTGTCACTACTCTGTGAGAAATGCTGAAATGAG  
5 GAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGAAATAG (SEQ ID  
NO: 246)

**AOLFR134 sequences:**

MTTILEVDNHTVTRFILLGFPTPAFOLLFFSIFLATYLLTLENLLLIHSDGQLHKPMYFFL  
10 SHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQLYFFVTFVCTEYILLAIMAFDRYVAIC  
NPLRYPMITNQLCGTLAGGCWFCGLMTAMIKMVFAQLHYCGMPQINHYFCDISPLLNVSC  
DASQAEMVDFFLALMVIAIPLCVVASYAAILATILRIPSAQGRQKAFSTCASHLTVVILFYSMT  
LFTYARPKLMYAYNSNKVVSVLYTVIVPLLNPIIYCLRNHEVKAALRKTHICRSGSPQGNAGFS  
S (SEQ ID NO: 247)

ATGACCACCATAAATTCTGGAAGTAGATAATCATACAGTGACAACACGTTTCATTCTTCTGG  
GGTTTCCAACACGACGACGCTTCCAGCTTCTCTTTTCTCCATTTTCTGGCAACCTATCTG  
CTGACACTGCTGGAGAATCTTCTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA  
AGCCCATGTACTTCTTCTGAGCCACCTCTCTCTGGAGATGTGGTATGTGACATGCATCATC  
15 AGCCCAAGATGCTTGTGACTTCTCAGTCATGACAAGAGTATTTCTCTCAATGGCTGCA  
TGACTCAACTTACTTTTGTGACCTTTGTCTGCACTGAGTACATCTCTTCTGCTATCATG  
GCCTTTGACCCGCTATGTAGCCATTGTAAATCCACTACGCTACCCAGTCAATGACCAAC  
AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTTCTGTGGACTCATGATGCCATGATTA  
20 GATGGTTTATATAGCACAACCTCACTACTGTGGCATGCCTCAGATCAACTCACTACTTTTGTG  
ATATCTTCCACTCTTAACGCTCTCTGTGAGGATGCCTCAGAGCTGAGATGGTGGACTT  
25 CTCTCTGGCCCTCATGTGCTATTGCTATTCTCTTTGTGTGTGGTGGCATCTCACTGCTCTA  
TCTTGTGCCACCATCTCAGGATCCCTTCTGCTCAGGGCCGCCAAAAGGCATTTCCACTGT  
TGCTTCCACCTGACCGTCTGAATTCTCTCTATTCATGACACTTTTCACTATGCCCGTC  
CCAAACTCATGTATGCTACAAATCCAAACAAAGTGGTATCTGTTCTCTACACTGTCATTGT  
30 CCATCTCTCAACCCCATCTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA  
AGACCATCATGTCAGAGGAAGTGGGCCCAAGGAAATGGGGCTTTCAGTAGTTAA (SEQ  
ID NO: 248)

**AOLFR135 sequences:**

MIFPSHDSQAFSTVDMEVGNCTILTEFILLGFSADSQWPILFGVFLMLYLIITLSGNMTLVILIRT  
35 DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASCVSSEDKRISLAGCGAQLFFSCVAYTECYLL  
AAMAYDRHAAICANPLLYSGMTALCTGLVAGSYIGFLNALAHTANFRLHFCGNIDHFFC  
DAPPLVKMSCNTNRYVEKVLGVVGGFVLSLAILISYVNILLAILRIHSAAGRHKAFSTCASHL  
ISVMLFYGSLFFMYSRPSTYSLERDKVAALFYTVINPLNPLIYSLRNKDIKAERKATQTIOQP  
40 T (SEQ ID NO: 249)

ATGATTTTCCCTTCTCATGATAGTCAGGCTTTACCTCCGTGGACATGGAAGTGGGAAAT  
GCACCATCTGACTGAATTCATCTTGTGGGTTTCTCAGCAGATTTCCAGTGGCAGCCGAT  
TCTAATTTGGAGTGTCTGATGCTCTAATTGATAACCTTGTGAGAAACATGACCTTGGTTA  
45 TCTTAATCCGAAGTATCCCACTTGCATACACCTATGTACTTTTCAATTGGCAATCTGTCT  
TTTTTGGATTTCTGGTATACCTCTGTGTATACCCCAAAATCCTGGCCAGTTGTGCTCAGA  
AGATAAGCGCATTTCTTGGCTGGATGTGGGGCTCAGCTGTTTTTCTGTGTTGTAGCCT  
ACACTGAAATGCTATCTCTGGCAGCCATGGCATATGACCCGCATGCAGCAATTTGTAACCC  
ATTGCTTTATTCAGGTACCATGTCCACCGCCCTCTGTACTGGGGCTGTGTCTGGCTCTCA  
50 TAGGAGGATTTTGAATGCCATAGCCCATAGCCCATACTGCCAATACATTCGCCCTGCAITTTGTGG  
TAAAAATATCATTGACCACTTTTCTGTGATGCACCAACCATTTGGTAAAAATGTCTCTGTACA  
AACACCAAGGCTACGAAAAAGTCTGCTTGGTGTGGGGCTCAGCACTACAGTACTTCAGCA  
TTCITGCTATCTGATTCTCATGTCAACATCTCTGCTGGCTATCTGAGAAATCCACTCAGCT  
TCAAGGAAGACAAAGGCATTCTCCACCTGTGCTTCCCACTCATCTCAGTCACTGCTCTTCTA  
55 TGGATCATTTGTGTTATGTATTCAAGGCCATAGTCCACCTACTCCCTAGAGAGGGACAAA  
GTAGCTGCTGTGTTCTACACCGTGATCAACCCACTGCTCAACCTCTCATCTATAGCTGAG

AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG  
A (SEQ ID NO: 250)

**AOLFR136 sequences:**

- 5 MTMENYSMAAQFVLDGLTQAEQLPLFLFLGIYVVTVVGNLGMILLIAVSPLLHTPMYYFL  
SSLSFVDFCYSSVITPKMLVNFGLGKNTILYSECMVQLFFVVFVVAEGVLLTAMAYDRYVAIC  
SPLLYNAMSSWVCSLLVLAFFLGLFSALTHTSAMMKLSFKCKSHIINHFFCDVLPDLLNSCSTN  
HLNELLFLIAGFNLTLPVLAVVSYAFILYSILHIRSSEGRSKAFGTCSHLMAVVIFFGSIIFY  
FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKNDVKALKRVLVVGK (SEQ ID NO: 251)
- 10 ATGACCATTGGAAAAATTATCTATTGGCAGCTCAGTTTGTCTTAGATGGTTAAACACAGCAAG  
CAGAGCTCCAGCTGCCCTCTTCTCTCTGTCTCTGGGAATCTATTGTGTCACAGTAGTGGG  
CAACCTGGGCATGATTCTCTGATTGCAGTCAGCCCTCTACTTACACCCCCATGTACTATT  
TCTTCAGCAGCTTGTCTCTCGTCGATTTCTGCTATTCCTCTGTGCATTACTCCCAAAATGCTG  
15 GTGAACATCTCAGGAAAGAAGAAATACAATCCTTTACTCTGAGTGTCATGGTCCAGCTCTTT  
TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACCTCTGACTGCCATGGCATATGATGCTA  
TGTGGCCATCTGTAGCCCATGCTTTATAATGCGATCATGTCTCATGGGTCTGCTCACTGTC  
TAGTGTCTGGTGCCTTCTTCTTGGGCTTCTCTCTGCTTGACTCATACAAGTGCCATGATG  
AAACTGTCTCTTTGCAAAATCCACATTATCAACCATTACTTCTGTGATGTTCTTCCCTCTCT  
20 CAATCTCTCTGCTCCAAACACACACCTCAATGAGCTTCTACTTTTATCATTCGCGGGTTTA  
ACACCTTGGTGCCCAACCTAGCTGTGTGCTGTCTCTATGCCCTCATCTCTACAGCATCTT  
CACATCCGCTCTCAGAGGGCGGTCCAAAGCTTTTGGAAACATGCAGCTCTCATCTCATGCT  
CTGTGGTGATCTCTTTGGGTTCATTACCTTCAATGATTTTCAAGCCCCCTTCAAGTAACCTC  
CTGGACCAAGGAGAAGGTGCTCTGTGTTCTACACCAACCGTGATCCCATGCTGAACCCCTT  
25 TAATATACAGTCAAGGAATAAGGATGTGAAGAAAGCATTAAGGAAAGGTCTTAGTAGGAA  
AATGA (SEQ ID NO: 252)

**AOLFR137 sequences:**

- 30 MSPENQSSVSEFLLGLPIRPEQAVFFALFLGMYLTTVLGNLIMLLIQLDLSHLHTPMYYFLSH  
LALTDISFSSVTPVKMLMNMQTQHLAVFYKGCISQTYFFIFADLDSLITSMAYDRYVAICHP  
HYATIMTQSCQVMLVAGSWVIACACALLHTLLLAQLSFCADHPIHYPCDLGALLKLSCSDSL  
NQLAIFTAALTAIMLPFLCILVSYGHIGVTILQIPSTGICKALSTCGSHLSVVTIYRTIIGLYFLP  
PSSNTNDKNIASVITA TPMNLNPIYSLRNKDIKALRKLSSRGAVAHACNLSLGG (SEQ  
ID NO: 253)
- 35 ATGAGCCCTGAGAACACAGCAGCGTGTCCGAGTTCTCTCTCTGGGCCCTCCCATCCGGC  
CAGAGCAGCAGGCGGTGTCTTCTCGCCCTGTCTCTGGGCATGTACCTGACCAACGGTGTCTGGG  
GAACCTGCTCATCATGCTGCTCATCCAGCTAGACTCTACCTTCACACCCCCATGTACTTCT  
40 TCCITAGCCATCTGGCCCTCACTGACATCTCCTTTTCACTGTGCATCTGTCCCTAAGATGCTG  
ATGAACATGCAGACTCAGCACTAGCCGTCTTTTACAAGGATGCATTTACAGACATATT  
TTTTCTATATTTTGTGCTGACTAGACAGTTTCTTATCACTTCAATGGCATATGACAGGAT  
GTGGCCATCTGTCATCTCTTACATTATGCCACCATCATGACTCAGAGCCAGGTGTGTCATGC  
TGGTGGCTGGGTCTCGGGTCATCGCTGTGCGGTGTGCTCTTTTGCAATACCCCTCTCTGGCC  
CAGCTTCTCTGTGCTGACCATCATCCCTCACTACTTCTGTGACCTTTGGTGCCTGTCT  
45 CAAGTTGTCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTTACAGCAGCATTGACA  
GCCATTATGCTTCAATCTCTGTGATCCTGGTTCCTTATGGTCACTTTGGGGTCAACCTCT  
CCAGATTCCCTCTACCAAGGGCATATGCAAGACCTTGTCCACTTGTGATGCCACCTCTCA  
GTGGTGACTATCTATTATCGGACAATATTGGTCTCTATTTTCTTCCCCCATCCAGCAACAC  
CAATGACAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTGTAAGAACCA  
50 TTCATTTACAGTCTGAGAAAAAAGACATTAAGGGAGCCCTAAGAAAACTCTTGAGTAGG  
TCAGGCGCAGTGGCTCATGCCGTGAATCTCAGCACTTTGGGAGGCTGA (SEQ ID NO: 254)

**AOLFR138 sequences:**

- 55 MLDNFDVTEFILLGLTSRREWQVLFVFLVYIITVVGNGIMMLLIKVSQPNLSPMYFFLSHLS  
FVDFVSSNVTPKMLNLSFDDKKTISYADLCAQCFIALVHVEIFLAAIAFDRTYTVGNPLLY  
GSKMSRGVCIRLITFPYIYGLTSLTATLWYTYGLYFCGKIEINHFCADPPLIKMACAGTFFVKEY

TMLLAGINFTYSYSLTVIIISYLFILJAILRMRSAEGRQKAFSTCGSHPTAVIIFYGTLIFMYLRRPTE  
ESVEQGKMOVAVFYFTTVPMLNPMIYSLRNKDVKKAMMKVIRSC (SEQ ID NO: 255)

5 ATGCTCAATTTACCGATGTGACAGAGTTCAATCTTTTGGGGCTAACGAGCCGTGCGGAAT  
GGCAAGTCTCTTCTTCATCGTTTTCTTGTGGTCTACATATACCCGTGGTGGCAATATC  
GGCATGTGTGTTGTTAACTCAAGGTCAAGTCCACAGCTTAACAGGCCCATGTACTTTTTCTCA  
GTCATCTGTCAATTTGTTGATGTGTGGTTTCTTCCAATGTACCCCTAAAAATGTTGGAAAT  
CTGTATTACAGATAAAAAACAAATTTCTATGCTGGCTGTTTAGCACAGTGTCTTCTTCAT  
10 TGCTCTGTGCCATGTGGAAATTTTATTCTGTGCTGCGATTGCCTTTGATAGATACACAGTGA  
TGGAAATCTCTTGTCTTTATGGCAGCAAAATGTCAAGGGATGTCTGATTTCGACGATTAC  
TTCCCTTACATTTATGGTTTCTGACGAGTCTGACAGCAACATTTAGGACTTATGGCTTGT  
ACTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT  
GGCCTGTGCCGGGACCTTGTAAAAGAAATACAAATGCTCATCTTGGCGGCATCAACTTC  
15 ACATATCCCTGACTGTAAATATCATCTCTTACTTATTCATCCCTCATTTGCCATTTCTGCGAAT  
GCGCTCAGCAGAAAGGAGGCAAGGCCCTTTCCACATGTGGGTCCCATCTGACAGCTGT  
CATCATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCCCAGGAGGATCTGTG  
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCAGTGTATCCCATGTTGAATCCCATGA  
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTATCAGCAGATCAT  
GTAA (SEQ ID NO: 256)

20 **AOLFRI39 sequences:**  
MGFPGIHSWQHWLSLPLALLYLLALSANILILIINKEAALHQPMYYFLGILAMADIGLATIMP  
KILAILWNAKTSLLSECFQMYAIHCFVAMESSTFVCMIAIDRYVAICRPLRYPISITSESVKAN  
GFMALRNSLCLISVPLLAQAQRHYCSQNGIEHCLSNLGVTSLSDDRRINSINQVLLAWTLMGS  
25 DGLILISYALISYVLKLSPEAASKALSTCTSHLILILFFYTVIIVISITRSTGMVRVPLIPVLNLV  
HNVIPPALNPMVYALKNKELRQGLYKVLRLGVKGT (SEQ ID NO: 257)

30 ATGGGATTCCCTGGCATTACAGTTGGCAGCACTGGCTCTCCCTGCCCTGGCTCTGCTCT  
ACCTCTTAGCTCTCAGTGCCAAACATCCTTATCCTGATCATCAACAAAGAGGCAGCACT  
GCACCAAGCTATGTACTTATCTTGGGCATCTTGGCTATGCCAGACATAGGCTGGCTACC  
ACCATCATGCCTAAGATTTTGGCCATCTTATGGTTCAATGCTAAGACCATCAGTCTCCTGG  
AGTGCTTTGGTCAGATGTATGCCATACATGCTTTGTGGCCATGGAATCAAGTACCTTTGT  
CTGATGGCTATTGATAGATATGTAGCCATTTGTGACCGCTACGATATCCATCAATCATC  
35 ACTGAATCTTTGTTTTCAAAGCAAATGGGTTTCATGGCACTGAGAAACAGCCTGTGTCTCA  
TCTCAGTGCCTCTGTTGGCTGCCAGAGCAATTACTGCTCCAGAAATCAAAATGAGCACTG  
TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAATCAATAGCAATT  
AACCAGGCTTTTGGCTGGACACTCATGGGAAGTACCTGGGTTTGATTTTATCAT  
ATGCTCTAATACCTTACTCTGTCTGAAGCTGAACCTCTCCAGAAGCTGCATCCAAGGCCT  
40 AAGTACCTGCACCTCCCACTCATCTTAATCCTTTCTTCTACACAGTCACTATTGTGATTT  
CCATTACTCGTAGTACAGGAATGAGAGTTCCTCTTATCCAGTCTACTAATGTGCTACACA  
CAATGTCAATCCCTCTGCCCTGAACCCCATGGTATATGCACTCAAGAAACAAGGAACCTCAGG  
CAAGGCTTATACAAGTACTTAGACTGGAGTGAAGGCACCTGA (SEQ ID NO: 258)

**AOLFRI40 sequences:**  
45 MLTLNKTDLPASFILVGPGLDQLWISFFPCSMYVYVAMVGNCGLLYLHIYEDALHKPMYY  
FLCMLSFDTLVMCSSTIPKALCIFWHLKDIGDECLVQMFHITFTGMESGVLMMLMDRYV  
AICVPLRSLTNPVIAKVGTATFLRGVLLIPFLLTKRLPYCRGNLPTTYCDHMSVAKLSG  
NVKVNIAVGLMVALLIGGFILCITISYTMILRAVVSLSADARQKAFNTCTAHICAIVFSYTPAF  
50 FSFFSHRFGHEHIIPPSCHIVANIYLLPPTMNPVYGVKTKQIRDCVIRLSGSKDKYSYSM (SEQ  
ID NO: 259)

ATGCTAACACTGAATAAAACAGACCTAATACCAGCTTCATTTATCTGAATGGAGTCCCAG  
GACTGGAAGACACACAACTCTGGATTTCCTTCCCATCTGCTCATGTATGTTGTGGCTAT  
GGTAGGGAATTTGGACTCCTCTACCTCATTCTACTATGAGGATGCCCTCAGCAAAACCTGAT  
55 TACTACTCTTGGCCATGCTTTTCTTACTGACCTTGTTATGTGCTCTAGTACAAATCCCTAA  
AGCCCTCTGCATCTTCTGGTTTCATCTCAAGGACATTGGATTGATGAATGCCCTGTGCCAG

ATGTTCTTCATCCACACCTTACAGGGATGGAGTCTGGGGTGCTTATGCTTATGGCCCTGG  
ATCGCATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCCTCACCACCTCTGTAATT  
GCAAGGTTGGGAGTGGCACTGCCACCTTCTGAGAGGGGTATTACTCATTTATCCCTTTACTTCTCT  
CACCAGCGCCTGGCCCTACTGACAGAGGCAATATACTTCCCCATACCTACTGTGACCACATG  
TCTGTAGCCAAATTGCTCTGTGGTAATGTCAAGGTCAATGGCATCTATGGTCTGATGGTTG  
CCCTCCTGATTTGGGGGCTTTGACATACTGTGTATCACCATCTCCTATACCATGATTCCTCGG  
GCAGTGGTTCAGCTCTCTCAGCAGATGCTCGGCAGAGGGCTTAAATACCTGCACTGCC  
ACATTGTGGCCATTGTTTCTCTATACTCCAGCTTCTTCTCCTTCTTTCCACCCTTTG  
GGGAACACATAATCCCCCTTCTTGGCCACATCTGTAGCCAAATTTATCTGCTCTACCA  
CCCATTGAACCTTATTGTCTATGGGGTGAAAACCAACAGATACGAGCATGTGTCATAA  
GGATCCTTTCAGGTTCTAAGGATACCAAACTCTACAGCATGTGA (SEQ ID NO: 260)

# **AOLFR141 sequences:**

MSSLGHNMESPNHTDVPDSVFLLGIPGLEQFHLWLSLPVCGLTATIVGNITLVVATEPVL  
HKPVYFLFCLMSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFHAFCCMMESTVLLAM  
AFDRYVAICHPLRYATILDTIIAHIGVAAVVRGSLMLPCPFLJRLNFCQSHVILHYTCGHMA  
VVKLAGCDTRPNRVVYGLTAAVLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVC  
VILISTPALFSFTHRFHHVVPVHIHILLANVYLLPPALNPVVYGVKTKQIRKRVVRVFQSGQ  
GMGIKASE (SEQ ID NO: 261)

ATGTCAGCAGCTCTTGGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCCTCTG  
TCTTCTTCTCTGGGATCCCAGGTCTGGAAACAAATTCATTGTGGTCTCAGCTCCCTGTG  
TGTGGCTTAGGCACAGCCACAATTTGGGCAATATAACTATTCTGGTTGTGTGTCACATG  
AACCAGTCTTGACAAAGCTGTGTACCTTTTCTGTGCATGCTCTCAACCATCGACTTGGCT  
GCCCTGTCTCCACAGTTCCCAAGCTACTGGCTATCTTCTGGGTGGAGCGGACATATAT  
CTGGCTCTGCTGCTGGCAGAGATGTTCTTCAATTCATGCTTCTGCAATGATGGAGTCCACT  
GTGCTACTGGCCATGGCCCTTTGATCGCTACGTGGCCATCTGCCACCCTCCGCTATGCCA  
CAATCTCTCACTGACACCATCATTTGCCACATAGGGGTGGCAGCTGTAGTGCAGAGCTCCCT  
GCTCATGCTCCCATGTGCCCTTCCTTATTGGGGCTTTGAACITCTGCCAAAGCCATGTGATCTC  
TACACAGCTACTGTGAGCACATGGCTGTGGTGAAGCTGGCTGTGGAGACACAGGCCCTA  
ACCTGCTGTATGGGGCTGACAGCTGCACTGTTGGTCATTGGGGTGACTTGTGTTGTCATTGG  
TCTCTCTTCCCTAAGTGCACAAGCTGTCTCTCGCCTCTCATCCCATGAAGCTCGGTCCA  
AGGCCCTAGGGACCTGTGGTTCCTATGTCTGTGTCATCTCATCTTATACACCTCCGCTCT  
TCTCTCTTTTATACACCGCTTTGGCCATCACGTTCCAGTCCATATTCACATCTTTTGGC  
CAATGCTTTATCTGCTTTTGGCCACTGCTCTTAATCTCTGTGATATGGAGTTAAGACCAAC  
AGATCCGTAAGAGAGTTGTCAAGGTGTTTCAAGTGGGCAGGGAATGGGCATCAAGGCAT  
CTGAGTGA (SEQ ID NO: 262)

# **AOLFR143 sequences:**

MLGLNGTFPQATILQLTGIPGIQTGLTWVALIFCILYMSIVGNLSILTLVFEPALHQPMMYYFL  
PMLANDLGVSFSTLPTVISTFCFNYNHVAFNACLQVQFFHITFSFMESGILLAMSLDRFVAICY  
SLRYVTVLTHNRLAMGLGILTKSFTTLFPFVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI  
HYNNIYGLLVIFTYGMDSIFILLSYALILRAMLVIIISQEQRLKALNTCMISHICAVLAFVYPIIIVS  
MIHRFWKSAAPPVVHVMMSNVYLVFPVPMNLPIIYSVKTEIRKGILKFFHKSQA (SEQ ID NO:  
263)

ATGCTGGGTCTCAATGGCAGCCCCCTCCAGCCAGCAACACTCCAGCTGACAGGCATTCTGT  
GGATACAAACAGGCCTCACCTGGGTGCCCCTGATTTCTGCATCCTCTACATGATCTCCATT  
GTAGGTAACCTCAGCATTTCTCACTCTGGTGTGTTGGGAGCCTGCTCTGCATCAGCCCATGT  
ACTACTTCTCTCTATGCTCGCTCTCAATGATCTGGGAGTGTCTTCTTACACTTCCCATCT  
GTGATTTCTACTTTCTGCTTCAACTACAACCATGTGCGTTAATGCTTGCTGGTGGTCCAGAT  
GTTCTTCATCCACACTTTCTCCTTCATGGAAGTCAGGCATACTGCTGGCCATGAGCTTGGATC  
GCTTTGTGGCTATTGTTATCCATTACGCTATGTCATGTGCTCACTCACAAACCGTATATG  
GCTATGGGTCTGGGCATCCTTACCAAGAGTTTCAACACTCTCTCCCTTTCCCTTTGTGGT  
GAAACGCACTGCCCTTCTGCAAAGGCAATGTTTGCATCACTCTCTACTGTCTCCATCCAGAT  
CTCATGAAAGTAGCATGTGGAGACATCCATGTTAACAACATTTATGGGCTCTTGGTGATCA

TTTTACCTATGGTATGGACTCAACITTCATCTGCTTTCCTACGCATTGATCCTGAGAGCC  
ATGCTGGTCATCATATCCCAGGAACAGCGGCTCAAGGCACCTCAACACCTGCATGCTACACA  
CTCTGTCAGTGTCTGGCCTTTATGTGCCATAATTGCTGTCTCCATGATTACACCGCTTCTGG  
AAAAAGTGCTCCACCTGTTGTTCATGTGCATGATGTCCAATGTCTACCTGTTTGTACCAACCAT  
5 GCTCAACCCATCATCTACAGTGTGAAACCAAGGAGATCCGCCAAAGGGATTCTCAAGTTCT  
TTCCATAAATCCCAGGCTGA (SEQ ID NO: 264)

**AOLFRI44 sequences:**

10 MGLFNVTHPAFLFLTGPGLLESSHWLSGPLCVMYAVALGGNTVLQAVRVEPSLHEPMMYYFL  
SMLSFSDAISMATLPTVLRFTCLNARNITFDACLIQMFLIHFFSMMESSGILLMSFDRYVAID  
PLRYATVLTTEVIAAMGLGAARSFTLFLPLFIKRLPICRSNVLSHSYCLHPDMMRLACADISI  
NSIYGLFVLVSTFGMDLFFHFLSYVLILRSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS  
TVHRFGKHVPCYHIVLMSNVYLFVPPVLPNLIYSAKTKEIRRAIFRMFHHIKI (SEQ ID NO: 265)

15 ATGGGGTGTTCATATGTCACTACCCCTGCATTCTTCTCCTGACTGGTATCCCTGGTCTGGA  
GAGCTCTCACTCCTGGCTGTCAAGGCCCTCTCGCTGATGTATGCTGTGGCCCTTGGGGGA  
AATACAGTGATCTTGCAGGCTGTGCGAGTGGAGCCAGCCTCCATGAGCCCATGTACTACT  
TCTGTGCTATGTTGCTCTTCACTGATGTGGCCATATCCATGGCCACACTGCCCATGTACTC  
CGAACCTTCTGCCATCAATGCCGCCCAACATCACITTTGTAGCTGTCTAATTCAGATGTTTCT  
20 TATTAACITCTCTTCCATGATGGAATCAGGATTCTGCTGGCCATGAGTTTTCACCGCTATG  
TGGCCATTGTGACCCCTTGGCGTATGCAACTGTGCTCACCCTGAAGTCATTGCTGCAAT  
GGGTTTAGGTGCAGCTGCTCGAAGCTTCATCACCCCTTTCCCTCTTCCCTTCTTATTAAAG  
GGCTGCCATCTCGAGATCCAATGTTCTTCTCACTCCTACTGCTGCACCCAGACATGATG  
AGGCTTGCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTTGTTCTTGTATCCAC  
25 CTTTGGCATGGACCTGTTTTTATCTTCTCCTATGCTGCTCAATTCGGTTCGTGCAATGG  
CCACTGCTTCCGCTGAGGAACGCCCTCAAAGCTCTCAACACATGTGTGTCACATATCCTGGC  
TGACTTCGATTCTATGTTGCAATGATTGGGGTCTCCACAGTGCAACGGCTTTGGGAAGCAT  
GTCCCATGCTACATACATGTCTCATGTCAAATGTGTACCTATTGTGCTCTCTGTGCTCAA  
CCCTCTCATTTATAGCGCCAAAGACAAAGGAAATCCGCCGAGCCATTTCCGCAATGTTTCAC  
30 CACATCAAAATATGA (SEQ ID NO: 266)

**AOLFRI45 sequences:**

35 MSVQYSLSPQFMILLSNITQFSPIFYLTSPFGLGKHWIFIPFFMYMVVAISGNCFLIIHKTNPRLH  
TPMYLLSLLALTDLGLCVSTLPTTMGIFWFSQSIYFGACQIQMFCHISFSFMESSVLLMMSFD  
RFVAICHLPLRVSIITGQVVRAGLIVIFRGPVATIPVILLKAFPYCGSVVLSHSFCLHQEVIQLA  
CTDITFNNLYGLMVVVFTVMDLVLIALSYGILHITVAGLASQEEQRRAFQTCTAHLCAVLV  
FVPMGLSLVHRFGKHAPPAIHLMLANVYLFVPPMLNPIIYSIKTKEIRRAIKLLGLKKASK  
(SEQ ID NO: 267)

40 ATGTCAGTCCAATATTCGCTCAGTCCTCAATTTCATGCTGCTATCCAACATTACTAGTTTATG  
CCCCATATCTATCTCACCAGCTTTCCTGGATTGGAAGGCATCAAACACTGGATTTCATCC  
CCTTTTCTTATGATACATGGTGTGCCATCTCAGGCAATGTGTTCAITCTGATCAITATTAAG  
ACCAACCCCTCGTGTGCAACACCCATGTACTTCTACTATCCTGTCTGGCCCTCACTGAGCT  
GGGGCTGTGTGTGTCACAGTGTGCCACCACATATGGGGATCTCTGGTTTAACTCCAGAGT  
45 ATCTACTTTGGAGCGGTGCAAAATCCAGATGTCTGCATCCACTCTTTTCTTTCATGGAGTC  
CTCAGTGTCTCATGATGTCTTGTACCGCTTTGTGGCCATCTGCCACCCCTCTGAGGTATT  
CGGTCAATTACATGCGCCAGCAAGTGGTCAGAGCAGGCTAATTGTATCTTCCGGGACCC  
TGTGGCCACTATCCCTATTGTCTCTCTCTGAAGGCTTTTCCCTACTGTGGATCTGTGGTCC  
TCTCCCACTCATTTTGCTGCACACGGAAGTGATACAGCTGGCCTGCACAGATACACACCTT  
50 CAATAATCTGTATGGAGTATGGTGGTAGTTTTCACGTGTGATGCTGGACCTGGTGCTCATC  
GCAGTGTCTATGGACTCATCTGTCACACAGTAGCAGGCTGGCCTCCCAAGAGGAGCAGC  
GCGGTGCTTTTCAGACATGCAACCGCTCATCTCTGTGCTGTGCTAGTATTCTTTGTGGCCAT  
ATGGGGCTGTCCCTGGTGCAACGTTTGGGAAGCATGCCCACTGCTATTCATCTTCTTAT  
GGCAATGTCTACCTTTTGTGCTCCCATGCTTAACCAATCATATACAGATTAAGACC  
55 AAGGAGATCCACCGTGCCATTATCAAACTCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ  
ID NO: 268)

**AOLFR146 sequences:**

- MSQVNTNTQEGYIITLDPGFEASHIWISIPVCCLYTISIMGNTILTIVRTEPSVHORMYLFSLM  
LALTDLGLTLTTLPTVMQLLWFNVRRISSEACFAQFFFLHGFSEFMESSVLLAMSVDVCYVAICCP  
5 LHYSILTNEVIGRTGLAIICCCVLAVLPSLFLKRLPFCCHSHLLSRSYCLHQDMIRLVCADIRLN  
SWYGFALALLIHVDPLLIVISYTLILKNILGTATWAERLRALNNCLSHILAVLVLYIPMVGVSMT  
HRFAKHASPLVHVIMANIYLLAPPVMNPITISVKNKQIQWGMNLNLSLKNMHRSR (SEQ ID NO:  
269)
- 10 ATGTCCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG  
GATTTTAGGGCCTCCCACATCTGGATCTCCATCCCCGTCTGCTGTCTTACACCATCTCCATC  
ATGGGCAATACCACCATCTCACTGTCAATTCGCACAGAGCCATCTGTCCACCAGCGCATGT  
ATCTGTTTCTCTCCATGCTGGCCCTGACGGACCTGGGTCTCACCCCTCACCACCTACCCACA  
15 GTCATGCAGCTTCTCTGGTTCAACGTTCTGTAAGTACAGCTCTGAGGCGCTGTTTGTCTCAGTT  
TTTCTTCTTCATGGATTCTCCTTTATGGAGTCTTCTGTCTCTGCTCCATGCTCAACATGAAGTCATTGGT  
GCTATGTGGCCATCTGCTGTCCCTCCATTATGCTCTCATCTCCAAATGAAGTCATTGGT  
AGAAGCTGGGTATGACCATCATTTGCTGCTGTGTTCTGGCGGTTCTTCCCTCCCTTTTCTTACT  
CAAGCGAGTGCCTTTCTGCCACTCCCACTTCTCTCTCGCTCCTAATGCTCTCCACAGGATA  
TGATCCGCTGGTCTGTGCTGACATCAGGCTCAACAGCTGGTATGGATTGCTCTTGCCCT  
20 GCTCATTTATATCGTGGATCCTCTGCTCATTTGTGATCTCCTATACACTTATCTGAAAAATA  
TCTTGGGCAAGCCACCTGGGCTGAGCGACTCCGTGGCCCTCAATAACTGCTGCTGCCACAT  
CTAGCTGCTCTGCTGCTCTCATCTCCATGGTGTGATCTATGACTCATGCTGTTTGCCA  
AGCATGCTCTCTCACTGGTCCATGTTATCATGAGCAATATCTACCTGCTGGCAGCCCCGGT  
GATGAACCCCATCATTTACAGTGTAAGAACAAGCAGATCCAAATGGGGAATGTTAAATTTT  
25 CTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

**AOLFR147 sequences:**

- MPSASAMIFIENLSSYNPGPFILVGIPGLEQFHVWIGIPFCIIYIVAVGNCILLYLIVVEHSLHEPMF  
FFLSMLAMTDLILSTAGVPKALSIFWLGAIREITPGCLTQMFFLHYNFVLDLSAILMAMAFDHYV  
30 AICSPRLRYTTLTPKTIKXAMGIFSRFCILPDVFLLTCLPFCRTRIIPHYCHIEHGVQAOLCADISI  
NEWYGFVCVPIMTVISDVILIAVSVAHILCAVGLPSQDACQKALGTGSHVCVILMFYTPAFSSI  
LAHRFGHNVSRTFHIMFANLYIVIPPALNPMVYGVKTKQIRDKVILFSGKTG (SEQ ID NO:  
271)
- 35 ATGCCATCTGCTCTGCCATGATCATTTTCAACCTGAGCAGTTACAATCCAGGACCCCTTCA  
TCTGTAGGGATCCCAGGCTGGAGCAATCCATGTGTGGATTGGAATCCCTTCTGTATC  
ATCTACATGTAGCTGTGTGGGAACTGCATCCTTCTCTACCTCATTTGTGGTGAGCATA  
GTCTTCATGAACCATGTCTCTTCTTCTCCATGCTGGCATGACTGACCTACATCTGTTC  
40 ACAGCTGTGTGCTCAAAGCACTCAGTATCTTTTGGCTAGGGGCTCGCGAAATCACATTC  
CAGGATGCCCTTACACAAATGTTCTTCTTCACTATAAATTTGTCTGGATTACGCCATCTG  
ATGGCCATGGCATTTGATCACTATGTAGCTATCTGTTCTCCCTTGAGATATACCACTCAT  
GACTCCCAAGACCATCATCAAGAGTGCTATGGGCATCTCCTTTCGAAGCTTCTGCATCAT  
CTGCCAGATGTATTCTGTGTCATGCTGCTGCTGCTGCTGATATCTCCATCAACTTCTG  
45 GTATGGCTTTGTGTGTCCCATCATGACGGTCATCTCAGATGTGATTTCTCATTTGCTGTTCT  
ACGCACACATCCTCTGTGCTGCTTTGGCCCTTCCCTCCCAAGATGCCTGCCAGAAAGCCCT  
CGGCATTTGTGGTCTCATGTCTGTGTCATCTCATGTTTATACACTGCTCTTTTCTCCA  
TCTCGCCCATCGCTTTGGACACAAATGTCTCTCGACCTTCCACATCATGTTTGCCAAATCT  
50 TACATTGTATCCCACTGCACTCAACCCATGGTTACGGAGTGAAGACCAAGCAGATCA  
GAGATAAGGTTATACCTTTGTGTTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

**AOLFR148 sequences:**

- MPTVNHSGTSHTVFHLGIPGLQDQHMWISIPFISYVALLGNSLLIFILTKRSLHEPMYLFCL  
MLAGADIVLSTCTIPQALAIWFWRAGDISLDRCTQLFHHSTFISEGILLVMAFDHYIAICYPLR  
55 YTTILNALIKCIVTVLSRSGYGTIFPIIFLLKRLTFCQNNIHPHTFCEHGLAKYACNDRIWYG



5 ATGCCTACTGTAAACCACAGTGGCACTAGCCACACAGCTCTTCCACTTGTGGGCATCCCTG  
GCCTACAGGACGACCATGTGGATTCTATCCATTCTTCACTGTACCGCCCTT  
CTTGGGAACAGCCTGCTCATCTCTATTATCTCAAAAGCGCAGCCTCAATGAACCCATGT  
ACCTCTTCTCTGCATGCTGGCTGGAGCAGACATGTCTCTTCCACGTGACCAATTCTCAG  
GCTTAGCTATCTTCTGGTTCGGTGTCTGGGACATCTCCTGGATCGTGTGCATCACTCAGCT  
10 CTTCTTCATCCATTCCACCTTCACTCTGTGAGTCAGGGATCTTGTGGTGTGGCCTTGACC  
ACTATATTGCCATATGCTACCCACTGAGGTACACCACTTCTTCAAAATGCTCTGATCAA  
GAAAATTTGTGTGACTGTCTCTGTGAGAAGTTATGTTACAATTTTCCCTATCATATTTCTT  
TAAAAGATTGACTTCTGCCAGAATAATATTATCCACACACCTTTGTGAACACATTGG  
CCTAGCCAAATATGCATGTAATGACATTCGAATAAACATTTGGTATGGGTTTTTCAATTCTA  
15 ATGTGCGACGGTGGCTTAGATGTTGTAATAATTTTATTTCTATATGCTGATTCTCCATG  
TGCTTCCACATGCTCTTCCAGATGCTTGGCACAAGCTCTCAACACATTTGGCTCCCATG  
TCTGCATCATCATCTCTTTATGGGTCTGGCATCTTCAACATCTTACCCAGAGGTTTGGGA  
CGCCACATTTCCACTGTATCCACATCCCGTGGCTAATGTCTGCAATTCTGGCTCCACCTAT  
GCTGAATCCCATTTATTTATGGGATCAAAACCAAGCAATCCAGGAACAGGTGGTTCAGTTT  
20 TTGTTTATAAACAGAAAATAACTTTGGTTAA (SEQ ID NO: 274)

**AOLFR149 sequences:**

MSNASLLTAFILMKPHAPALDAPLFGVFLVVYLVTLGNLILLVIRVDSHLHTTMYFYLTNL  
SFIDMGVSTVTVPKLMLTLVFPSGRAISFHSMAQLYFFHFLGGTECFLYRVMSCDRYLAISSP  
LRYTSMVMTGRSCITLLATSTWLSGSLHSVAQAILTFHLPYCGPNWQHLYCLDAPPILKLACADTS  
25 ALETVFMTVGVIGASGCFVLIVLSYVSIVCSILRIRTSSEGHRAFOCTCAASHIVLCCFFGPGLFYLR  
PGSRKAVDGVVAVFYTVLTPLLNPVYVTLRNEVKKALLKLKDKVAHSQSK (SEQ ID NO:  
275)

30 ATGTCCAACGCGCAGCTTACTGACAGCGTTTCACTCTATGGGCTTCCCCATGCCCAAGCGC  
TGGACGCCCCCTCTTTGGAGTCTTCTGGTGTTCACGTGCTCACTGTCTGGGGAACCT  
CCTCATCTCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCACCATGTACTACTTCTCA  
CCAACTGCTGCTTCAATGACATGTGGTCTTCCACTGTGACGGTGCCCAAATTTGCTGATGAC  
TTTGGTGTCCCAAAGTGGCAGGGCTATCTCTTCCACAGCTGCATGGCTCAGCTATTTCT  
35 TTCACTTCTTAGGGGGCACCAGAGTGTCTCTTACACAGGTCATGTCTGTGATCGCTACCT  
GGCCATCAGTTACCGCTCAGGTACACCATGATGACTGGGCGCTCGTGTACTCTTCTG  
GCCACCAGCACTTGGCTCAGTGGCTCTCTGCATCTGTCTGCCAGGCCATATTGACTTTCC  
ATTGGCCCTACTGTGGACCACTGGATCCAGCACTATTGTGTGATGACACCGCCATCTCT  
GAAACTGGCCTGTGCAGACACCTCAGCCATAGAGACTGTCAATTTTGTGACTGTTGGAATA  
GTGGCCTCGGGTCTGCTTGTCTGATAGTGTCTCATGTGTCCATGCTCTGTCCATCTCT  
40 CGGGATCGCGACCTCAGAGGGGAAGCAGAGCCTTTCAGACCTGTGCTGCTCCCACTGATC  
GTGGTCTCTTGTCTCTTGGCCCTGGTCTTTTCACTTTACCTGAGGCGCAGGCTCCAGGAAAGC  
TGTGGATGGAGTTGTGGCCGTTTTCACACTGTGCTGACGCCCCCTTCTCAACCCCTGTGTGT  
ACACCCTGAGGAACAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAGACAAAGTAGCAC  
ATTCTCAGAGCAAAATAG (SEQ ID NO: 276)

45

**AOLFR150 sequences:**

MELGNVTRVKFIFLGLTQSQDQSLVLFCLVYMTLLGNLIMVTVTCESRLHPTMYFYLLR  
NLAILDICFSSTTAPKVLDDLKSKKTISYTSMTQIFLHLLGGADIFSLSVMAFDYMAISKPL  
HYVTIMSRGQCTALISASWMGGFVHSIVQISLLPLPCGPNVLDTFYCDPVQVLKLTCTDTFA  
50 LEFLMISNGLVTTTWIFLLVSYTVILMTLSRQAGGGRRAIKSTSPHKGCDPAFCALHCLCLC  
PALHCPPHRKGHLCILHCHLPSAEFPLDHSSEPGNEVSHKEETEEKTRAF (SEQ ID NO: 277)

ATGGAGTTGGGAAATGTCACCAGAGTAAAGAAATTTATATTTCTGGGACTTACTCAATCCC  
AAGACAGAGATTGGTCTTGTCTTTTATATGCTCTGTGATACAGCACTCTGCTGGGA  
AACCTCTCATCTGCTCACCGTGACCTGTGAGTCTCGCATCCACACCCTATGACTTCTCT  
GCTCGCAATCTAGCCATCTTGTACATCTGCTTCTCTCCACAACCTGCTCTAAAGTCTTGC

5 TGGACCTTCGTCAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATATTTCT  
CTTCCACCTCCTTGGTGGGGCAGACATTTTTTCTCTCTGTGATGGCGTTTGACTGCTACA  
TGGCCATCTCCAAGCCCTGCACATGTGACCATCATGAGTAGAGGVMCAATGCATGCGCT  
CATCTCTGTCCCTCTTGGATGGGGGGCTTTGTCCACTCCATCGTGCAGATCTCCCTGTGTGCTGC  
10 TCTTCCCTTTCTGTGACCCCAATGTCTTGACACTTTCTACTGCGATGTCCCCAGGTCCTC  
AAACTCAGCTTGCATCTGACACATTTTGTCTTGAGTCTTGATGATTTCCAACAATGGGCTGGT  
CACTACCTGTGGTTTATCTTCTGCTTGTGTCTACACAGTCACTCCTAATGACGTGTAGGT  
CTCAGGCAGGAGGGGGCAGGAGGAAAGCCATCTCCACTGCACTCCCCACATCACTGTG  
GTGACCTTGCATTTTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCAC  
AGAAAAGGCCATCTCTGCACCTTCACTGTCACTTCCCTCTGTGAAACCCCTTGATCTACA  
CTCTGAGGAACCAAGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTGTGCGCTT  
CTGA (SEQ ID NO: 278)

**AOLFR151 sequences:**

15 MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLITLAGNLCMILLIRTNHSLQTPMYFFLGLHS  
FVDICYSSNVTNMLHNFLSEQKTI SYAGCFTQCLLFLALVITEFYLILASMLDRYVAICSPHYHS  
SRMSKNICVCLVTIPYMYGFLSGFSQSLTTFHLSFCGSLINHFIYCADPPLIMLACSDTRVKKMA  
MFV VAGFNLSSLLFIILLSYLFI FAFIRISAEGRHKAFSTCASHLITVTLFYGTLCFMYVRPPE  
KSVESKITAVFYTFSLPMLNPLIYSLRNTDVLAMQMQIRGSKSFHKIAV (SEQ ID NO: 279)

20 ATGTTCTCCCCAAACCACCATAGTGACAGAATTCATCTCTTGGGACTGACAGACGACC  
CAGTGCTAGAGAAGATCTGTTTGGGGTATTCCTTGCATCTACCTAATCACTGCGCAGG  
CAACCTGTGCATGATCTGCTGATCAGGACCAATCCCACTGCAAAACACCCATGATTTCT  
TTCCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTCCAATGTTACTCCAATATGTCT  
25 GCACAATTCCTCTCAGAACAGAACACCATCTCCTACGCTGGATGTTCCACAGTGTCTT  
CTCTTCACTGCCCTGGTGATCACTGAGTTTACCATCTTGTCTCAATGGCATGGATCGCTA  
TGTAGCAATTTGACGCCCTTGCATTACAGTTCAGGATGTCCAAGAACATCTGTGTCTGT  
CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTCTCTCAGTCACTGCTAACCTT  
TCATCTATCTCTGTGGCTCCCTTGAATCAATCATTCTACTGCGCTGATCTCTCTTCTA  
30 TCATCTGGCTGCTGCTGACACCCGTGTCAAAAGATGGCAATGTTGTAGTGTGAGGCTT  
TAATCTCTCAAGCTCTCTCTTATCATTTCTTCTGCTATCTTTTCAATTTTGTGAGCGATCT  
CAGGATCCGTTCTGTGAGGCAAGGACAAAGCCTTTCTACGTGTGCTTCCCACTGACA  
ATAGTCAATTTGTTTATGGAACCCCTTCTGCACTGACGTAAAGCCCTCAACAGAGAAGT  
CTGTAGAGGATGCCAAATAAAGTGCAGTCTTTATACCTTTTGTAGCCCAATGCTGAACCC  
35 ATTGATCTATAGCCTACGGAACACAGATGTAATCCTTGCCATGCAACAAATGATTAGGGGA  
AAATCCTTTACATAAATGTCAGTTTAG (SEQ ID NO: 280)

**AOLFR152 sequences:**

40 MDQINHNTNVEFFFLFELRSREFFLVVFFVYVATVLGNALIVVTITCESRLHTPMYFLLRN  
KSLVDIVFSSITVPKFLVDLLSDRKTI SYNDCAQIFFFFHAGGADIFFLSVMAYDRYLAIKPL  
HYVTMMRKEVWVALVVASWVSGGLHSIIQVILMLPFPFCGPNLTDAFYCYVLQVVKLACTDT  
FALELFMSNGLVTLWFLLLGSYTVILVMLRSHSGEGRNKALSTCTSHMLVVTLHFVPCV  
YIYCRPFMTLPMDTTISINNTVITPMLNPIIYSLRNQEMKSAMQRLQRLGPSESRRKWG (SEQ ID  
NO: 281)

45 ATGGACCAGATCAACCACACTAATGTGAAGGAGTTTTTCTTCTGGAACCTTACACGTTCCC  
GAGAGCTGGAGTTTTTCTTGTGTGCTCTTCTGCTGTATGTAGCAACAGTCTGGG  
AAATGCACCTCATTTGTGTCCTATTACCTGTGAGTCCCGCTACACACTCCTATGTACTTTC  
50 TCCTGCGGAAACAAATCAGTCTGTGACATCGTTTTTCACTATACACCGTCCCCAAGTCTCTGT  
TGGGATCTTTTATCAGACAGGAAACCATCTCCTACAATGACGTGATGGCACAGATCTTTT  
TCTTCCACTTGTCTGTGGGGCAGATATTTTTTCTCTCTGTGATGGCCTGTGACAGATAC  
CTTGCAATTCGCCAAGCCCTGCACTATGTGACATGATGAGGAAAGAGGTGTGGGTGGCC  
TTGGTGGTGGCTTCTGGGTGAGTGGTGGTTTGCAATCAATCCAGGTAATCTGTAGTGT  
TTCATTTCCCTCTCTGTGCCCAACACACTGGATGCCTTCTACTGTGTATGTCTCCAGGTG  
55 GTAAAACCTGGCTGCACTGACACCTTTGCTTTGGAGCTTTTCATGATCTCTAACACCGGAC  
TGGTGACCTGCTCTGGTTCCTCTGCTCTGGGCTCTACACTGTCACTTCTGGTGTGCTGT

AGATCCCACTCTGGGGAGGGGGCGGAACAAGGCCCTCTCCACGTGCACGTCCACATGCTG  
GTGGTGACTCTTCACTTCGTGCCTTGTGTTACATCTACTGCCGCCCTTCATGACCGTGCC  
CATGGACACAACCAATATCCATTAAATAACACGGTCAATACCCCATGCTGAAACCCCATCATC  
TATTCCTCGTAGAAATCAAGAGATGAAAGTCAGCCATGCAGAGGCTGCAGAGGAGACTTGGG  
CCTTCCGAGAGCAGAAAATGGGGGTGA (SEQ ID NO: 282)

# **AOLFR153 sequences:**

MSKTSLVTAFFILGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILVIRVDSHLHTPMYYFLTNLS  
FIDMWFSTVTVPKMLMTLVSFSGRAISHSCVAQLYFFHFLGSTCEFLYTVMSYDRYLAIASPL  
RYTSMMSGRCALLATSTWLSGSLHSAVQTILTHFLPYCGPNQIQHLYLVDAPPLKLACADTSA  
NEMVIFVDIGLVASGCFLLIVLSYVSIVCSILRIHTSEGRHRAFQTCASHCIVLFCFVXCVFIYLR  
PGRDVVVDGVVAIFYTVLTPLLNPVVYTLRNKEVKKAVLKLDRKVAHSQGE (SEQ ID NO:  
283)

ATGTCCAAGACCAGCCTCGTGACAGCGTTATCCTCACGGGCCTTCCCATGCCCCAGGGC  
TGGACGCCCACTCTTTGGAATCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT  
CCTCATCTCGTGTGATGACAGGGTGGATTCTCACCTCCACACCCCATGTACTACTTCTCA  
CAACCTGTCTCTTACATGATGTTCTTCCACTGTACGGTGCCCAAAATGCTGATGAC  
CTTGTTGTGCCAACGGCGCAGGGCTATCTCCTTCCACAGCTGGTGGCTCAGCTCTATTTT  
TCCACTCTGGGGAGCACCGAGTGTCTTCTCTCACAGTCATGTCTATGATCGACTCTTG  
GCCATCAGTTIACCCGCTCAGGTACACCGCATGATGAGTGGGAGCAGATGTGCCCTCTTG  
CCACAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT  
TTGCCCTACTGTGGACCAACAGAGATCCAGCACTATTGTGTAGTCACCGCCCATCTGA  
AATGGCTGTGACAGACCTCAGCCAACGAGAGTGGTCATCTTTGTGGACATTGGGCTAGT  
GGCTCGGGGCTGTTCTCTGATAGTGCTGTCTTATGTGCCATCGTCTGTTCATCCTGC  
GGCTCAGCACTCAGAGGGGAGGCGACAGAGCCTTTCAGACCTGTGCCCTCCCATGCACTGT  
GGTCTTTGCTTTTGTNNCTGTGTTTTCATTTTACCTGAGACCGGCTCCAGGAGCGTGTG  
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACACCCCTTCTCAACCTGTGTGTAC  
ACCTGAGAAACAAAGGAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACAT  
TCTCAGGGAGAAATAA (SEQ ID NO: 284)

# **AOLFR156 sequences:**

MCWAMPSPFTGSSTRNMESNRNQSTVTEFIFTGFFQLQDGSLLYFFPLFIYTHIIDNLLIFSAVRL  
DTHLGNPMYNFISIFLEIWTATIPKMLSNLISEKKAISMGTGILQMYFFHLSLESEGILLTT  
MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCFLGFLLPEIVMISTLPFCGPNQIQHIFCDLVP  
VLSLACTDTSMLIEDVIAHVTHITFLIALSYVRIVTVILRIPSSSEGRQKAXSTCAGHLMVFLFFG  
VSLSMYLRFNSTYPPVLDIAIALMFTVLAPFFNPIHYSLRNKMNMNAIKKLFCLQKVLNKPGG  
(SEQ ID NO: 285)

ATGTGCTGGGCTATGCCCTTCCATTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA  
ACCAATCAACAGTGACTGAATTTATCTTCACTGGAATCCCTCAGCTTCAGGATGGTAGTCT  
CTGTACTTCTTCTCTTACTTTTCACTATACTTTTATATCAATTGATAACTTATTAATCTT  
CTGTGCTAAAGGCTGGACACCATCTGGGCAACCCCATGTATAATTTTATCAGTATATTTT  
CCTTCTGGAGATCTGGTACACCACAGCCACCATTCCTCAAGATGCTCTCCAACTCATCAG  
TGAAAAGAAAGGCCATCTCAATGACTGGCTGCATTTGCAGATGTAATTTCTTCCACTCACTT  
GAAAAGCAGAGGGGATCTGTGTGACCACCATGGCCATTGACAGATACGTTGCCATCTGCA  
ACCTTCTCGCTATCAATGATCATGACCCCCGGCTCTGTGCTCACTCTTCAGGTTCC  
TGCTCTTCGGTTTCTTATCTGCTTCCGAGATTGTGATGATTTCCACACTGCCTTTCTGT  
TGGGCCCAACCAATTCATCAGATCTCTGTGACTTGGTCCCTGTGTGAAGCTGGGCTGT  
ACAGACAGCTGCATGATTCGATTGAGGATGTGATTCATGCTGTGACCATCATCAATTA  
TCCTAATCATTTGCCCTGTCTATGTAAGAAATTTGCTCACTGTGATATGAGGATTCCTCTTCT  
GAAGGGAGGCAAAAGGCTNTTTCTACCTGTGCAGGCCACCTCATGGTCTTCTCGTATTAITCT  
TTGGCAGTGTACTCATGTACTTGCCTTTCAGCAACACTTATCCACCAGTTTGGACAC  
AGCCATTGCATGATGTTTACTGTACTTGTCTCAATTTCTCAATCCCATCATTTATAGCCCTGA  
GAAACAAGGACATGAACAATGCAATTAATAAACTGTTCTGTCTTCAAAAAGTGTGGAACA  
AGCCTGGAGGTTAA (SEQ ID NO: 286)

**AOLFR157 sequences:**

MAMDNVTA VFQFLLIGNSY PQWRDTFFTLVLIIYLLSTLLNGFMIFLIHFDPNLHTPIYFLLSNL  
5 SFLLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLLAAMAYDRVVAINSNP  
LRYSVVMNGPVCVCLVATSWGTSVLVTAMLJLSRLHFCGANVINHFACELLSLIKLTCSDTSL  
NEFMILITSITLLLPFGFVLLSYIRIAMAIIRISLQGRLLAFTTCGSHLTVVTIFYGSAISMVMYKT  
QKSSPPDQDKFISVFY GALTPMLNPLIYSLRKKDVKAIRKVM LKRT (SEQ ID NO: 287)

10 ATGGCCATGGACAATGTCACAGCAGTGTTTCAGTTTCTCCTTATTCGGCATTCTCAACTATCC  
TCAATGGAGAGACACGTTTTCACATTAGTGCTGATAATTTCACAGCACATTGTTGGGG  
AATGGATTTATGATCTTCTTCAITTCACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT  
CCTTAGTAACCTGTCTTCTTAGACCTTGTATTGGAACAGCTTCCATGCCCCAGGCTTTGG  
TGCAITGTTTCTCTACCCATCCCTACCTCTCTATCCCGATGTTTGGCTCAAACGAGTGTC  
15 TCTTGGCTTTGGCCACAGCAGAGTGCCCTCTACTGGCTGCCATGGCCTATGACCGTGTGG  
TTGCTATCAGCAATCCCCTGCGTTATTCAAGTGTTATGAATGGCCAGTGTTGTCTGCTT  
GGTIGCTACCTCATGGGGGACATCACTTGTGCTCACTGCCATGCTCATCTATCCTCGAGG  
CTTCACCTCTGTGGGGCTAATGTCATCAACCAATTTTGCTGTGAGATCTCTCCTCATTAAG  
GTGACCTGTTCTGATACCAGCCTCAATGAATTTATGATCCTCATACCCAGTATCTTCAACC  
20 TGCTGCTACCAITTTGGGTTTGTCTCCTCTCTACATACGAAATGTGATGGCTATCATAAAGG  
ATTGCTCACTCCAGGCGAGGCTCAAGGCTTTACCACATGTGGCTCTCACTGACCGCTGG  
TGACAATCTTCTATGGGTGAGCCATCTCATGTATATGAAAACCTACGTCCAAGTCTCCCC  
TGACCAGGACAAGTTTATCTCAGTGTTTATGGAGCTTTGACACCCATGTTGAACCCCTCG  
ATATATAGCCTGAGAAAAAAGATGTTAAACGGGCAATAAGGAAAGTTATGTTGAAAAGG  
ACATGA (SEQ ID NO: 288)

25

**AOLFR158 sequences:**

MKAGNFSDTPEFFLL LSGDPELQILFMLFLSMYLA TMLGNLLIILAVNSDSLHTPMYFLLSI  
LSLVDFICTSTTTPMKMLVNIQAQSQSINYTGCLTQICFVLVFGLENGILVMMAYDRFVAICHP  
30 LRYNVIMNPKLCGLLLLSFIVSVLDALLHTLMVLQLTFCIDLIEPHFCELAHLKLACSDVLIN  
NILVYLVTSLLGVPLSGHFSYTRIVSSVMKIPSAAGKYKAFSCSHLIVVSLFYGTGFGVLYSS  
GATHSSRKGAIASVMTYVTPMLNPLIYSLRNKMDMLKALRKLISRPSFH (SEQ ID NO: 289)

35 ATGAAAGCAGGAACTTCTCAGACACTCCAGAAATCTTTCTCTTGGGATTGTCAGGGGATC  
CGGAGCTGCAGCCCATCCTCTCATGCTGTTCTGTCATGTACCTGGCCACAATGCTGGG  
GAACCTGCTCATCATCTCGGCCGTCAACTCTGACTCCCACCTCCACACCCCATGATCTCC  
TCCTCTCATCTCCTGCTTGGTCGACATCTGTTTCACTCCACACGATGCCAAAGATGCTG  
GTGAACATCCAGGCAAGGCTCAATCCATCAATTACACAGGCTGCCTACCCCAATCTGCT  
TTGCTCTGGTTTGTGGATTGGAAAATGGAATCTGGTCATGATGGCTATGATCGATT  
40 TGTGGCCATCTGTCAACCCATGAGGTACAATGTATCATGAACCCCAAACTCTGTGGGCTG  
CTGCTTCTGCTGCCTTCATCGTTAGTGCTCGGATGCTCTGCTGCACACGTTGATGGTGCT  
ACAGCTGACCTTCTGCATAGACCTGGAAATCCCCACTTTTCTGTGAACCTAGCTCATATTC  
TCAAGCTCGCCTGTCTGATGTCTCATCAATAACATCCTGGTGATTTGGTGACCGACT  
GTTAGGTGTGTTCTCTCTCTGCGGATCATTTTCTCTTACACACGAATGTCTCTGTGCA  
45 TGAATAATCCATCAGCTGGTGGAAAGTATAAAGCTTTTCCATCTCGGGGTACATTAACT  
CGTTGTTTCTGTTTATGGAACAGGCTTGGGGTGACCTAGTTCTGGGGCTACCCACT  
CCTCCAGGAAGGGTCAATAGCATCAGTGATATACCGTGGTCAACCCCATGCTGAACCC  
ACTCATTTACAGCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAACTAATATCTAG  
GATACCATCTTCCATTGA (SEQ ID NO: 290)

**AOLFR159 sequences:**

50 MGPRNQTA VSEFLMKVTEDELPKLIPFLSFLSMYLVTLGNLLILLAVISDSLHTPMYFLLFN  
LSFTDICLITTTVPKILVNIQAQSQSITYTGCLTQICLVLVFGLESCLFVAMAYDRYVAICHP  
RYTVLMNVHFVGLLILSMFMSTMDALVQSLMVLQSFCKNVEIPLFFCEVVQVIKLACSDTL  
INNILIFYASSVFGAIPLSGHFSYQIVTSVLRMPARSARGKYKAFSTCGCHLSVFSFLFYGTAFGVYIS  
55 SAVAESSRITAVASVMTYVTPQMMNPFYSLRNKEMKALRKLIGRLPFF (SEQ ID NO: 291)

ATGGGACCCAGAAACCAACAGCTGTTTCAGAATTTCTTCTCATGAAAGTGACAGAGGAC  
 CAGAAGCTGAAGTTAATCCCTTCAGCCTGTTCTGTCCATGTACCTGGTACCATCCTGG  
 GGAACCTGCTCATTTCTCCTGGCTGTCATCTCTGACTCCACCTCCACACCCCATGTACTTC  
 CTCTCTTTAATCTCTCCTTTACTGACATCTGTTTAAACACAACCAAGCTCCCAAGATCCT  
 5 AGTGAACATCCAAGCTCAGAATCAGAGTATCACTTACACAGGCTGCCTACCCAGATCTGT  
 CTGTGCTTGGTTTTTGTGGCTTGGAAAGTTGCTTCTTGACAGTCATGGCCTACGACCCGTA  
 TGTGGCCATTGTGCCACCCACTGAGGTACACAGTCCATGAATGTCCATTTCTGGGGCTTG  
 CTGATCTTCTCTCCATGTCATGAGCACTATGGATGCCCTGGTTACAGAGTCTGATGGTATT  
 GCAGCTGTGCTCTCTGCAAAAACGTTGAAATCCCTTTGTCTTCTGTGAAGTCGTTACAGGTC  
 10 ATCAAGCTCGCCTGTTCTGACACCCCTCATCAACAACATCCTCATATTTTGGCAAGTAGTGT  
 ATTTGGTGCAATTCCTCTCTCTGGAATAATTTTCTCTTATTTCAAAATGACCTCTGTTTC  
 TGAAATGCCATCAGCAAGAGGAAAGTATAAAGCGTTTTCCACCTGTGGCTGTACCTCTC  
 TGTTTTTTCTTGTCTATGAGGACAGCTTTTGGGGGTGTACATTAGTTCTGCTGTTGCTGAGT  
 CTTCGCCAATTACTGCTGTGGCTTCAAGTATGTACACTGTGGTCCCTCAAAATGATGAACCC  
 15 CTTTCATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGAAACTTATGGTAG  
 GCTGTTTCCTTTTAG (SEQ ID NO: 292)

**AOLFR160 sequences:**

MPMQLLLTDFIIFSIRFIINSMEARNQTAISKFLLLGLIEDPELQPVFLSFLSMYLVTLGNLILL  
 20 AVISDSHLHTPMYFFLSNLSFLDICLSTTTTPKMLVNIQAQNRSTYSGLTQICFVLFAGLENC  
 LLAAMA YDRYVAICHPLR YTVIMNPRLCGLLILLSLTSSVNNALLSLMLVRLSFCTDLEIPLF  
 CELAQVIQLTGSDTLINILNYFAACIFGGVPLSGHILSYTQITSCVLRMPSPASGKHKA VSTCGSHL  
 SIVLIFYGAGLGVISVSVTDSRKTAVASVMYSVFPQMVNPFYISLRNKMKGTLRKFGRIP  
 SLLWCAICFGFRFLE (SEQ ID NO: 293)

ATGCCGATGCAGCTGCTGCITACAGATTTTATTATCTTTTCCATCAGATTTCATCATCAACAG  
 CATGGAAGCGAGAAACCAACAGCTATTTCAAAATTCCTCTCTCGGACTGATAGAGGAT  
 CCGGAACCTGCAGCCCGTCTTTTACGCCGTCTCTGTCCATGTACTTGGTACCATCTCGGG  
 30 GAACCTGCTCATCTCTTGGCTGTATCTCTGACTCTCACCTCCACACCCCATGTACTTCT  
 TCCTCTCCAATCTCTCTTTTGGACATTGTITTAAGCACAAACACGATCCCAAGATGCTGT  
 GTGAACATCCAAGCTCAGAATCGGAGCATCACTGACTCAGGCTGCCTACCCAGATCTGCT  
 TTGTCTGTITTTTGTGCTGGCTTGGAAAATGTCTCCTTGCAAGCAATGGCCTATACCCGCTAT  
 GTGGCCATTGTGCAACCCCTTAGATACACAGTCATCATGAACCCCGCCTCTGTGGCCTCG  
 TGATTCCTCTCTCTCTGTGACTAGTGTGTGAATGCCCTTCTCTCAGCTGATGGTGTTG  
 35 AGGCTGTCTCTCTGTCACAGACCTGGAATCCCGCTCTTCTTCTGTGAACCTGGCTCAGGTCA  
 TCCAACCTACCTGTCTCAGACACCTCATCAATAACATCTGATATATTTGACAGTCTGCATA  
 TTTGGTGGTGTTCTCTGTCTGGAATCATTTTGTCTTACACTCAGATCACTCTGTGTTTT  
 GAGAATGCCATCAGCAAGTGGAAGCACAAAGCAGTTTCCACCTGTGGGTCTCACCTCTCC  
 ATTGTTCTCTTGTCTTATGGGGCAGGTTTGGGGGTGTACATTAGTTCTGTGGTTACTGACT  
 40 ACCTAGGAAGACTGCAGTGGCTTCAAGTATGTATCTGTGTCTCCTCAAAATGGTGAACCC  
 TTTATCTATAGTCTGAGGAATAAGGACATGAAGGAACCTTGAGGAAGTTCAATAGGAGG  
 ATACCTCTTCTCTGTGGGTGTGCCATTGTCTTGGATTACAGTTTCTAGAGTAA (SEQ ID  
 NO: 294)

**AOLFR161 sequences:**

MEPRNQTSASQFILLGLSEKPEQETLLFSLFFCMYLMVMVGNLLIILAIISIDSHLHTPMYFFLANL  
 SLVDVCLANTNTPKMLVSLQTGSKAISYPCCLIQMYFFHFGIVDSVIAMMAYDRFVAICHPLH  
 YAKIMSLRLCRLVLNGLWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCDTSVNR  
 IFILIVAGMVIATPFVICILASYARILVAIMKVPSAGGRKAFSTCSSHLSVVALFYGTIGVYVLCF  
 50 SSVLTVTVEKASAVMYTAVTPMLNPFYISLRNRDLKGALRKLVRNKITSSS (SEQ ID NO: 295)

ATGGAACCAAGAAACCAACAGTGCATCTCAATTCATCTCTCTGGGACTCTCAGAAAAGC  
 CAGAGCAGGAGACGCTTCTCTTTCCCTGTTCTTCTGTCATGTACCTGGTCACTGGTCTGGG  
 GAACCTGCTCATATCTCTGGGCAACGATAGACTCCACCTCCACACCCCATGTACTTCT  
 55 TCCTGGCCAACTGTCCCTGGTGTGATTCTGTCTGGCCACCAACACCATCCCTAAGATGCT  
 GGTGAGCCTTCAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCTGATCCAGATGTAC

5 TTCTTCCATTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGACCGGTT  
 CTGGGCGCATCTGCCACCCATTGCCACTACGCCAAGATCATGAGCCTACGCCTCTGTCCGCTG  
 CTGGTCGGCGGCCCTCTGGGCGTTTTCCTGCTTCATCTCACTCACTACATCTCCTGATGGC  
 CCGTCTCGTTTTCTGCGGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC  
 10 TCCGACTTTCTGTCACGGGACCTCTGTGAATAGGATTTTCATCTCTCATTGTGGCAGGGAT  
 GGTGATAGCCACGCCCTTTGTCTGCATCTTGGCCTCCTATGCTCGCATCTCTGTGGCCATCA  
 TGAAGGTCCCTCTGACGGCGGCAGGAAGAACGCTTCTCCACCTGCAGCTCCACCTCTGCT  
 TGTGGTTGCTCTCTTCTATGGGACCACCATTTGGCGTCTATCTGTGTCCTCTCGGTCTCTCA  
 CCACTGTGAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCAACCCCATGCTGAATCC  
 CTTCATCTACAGCTTGAGGAACAGAGACCTGAAAGGGGCTCTCAGGAAGCTGGTCAACAG  
 AAAGATCACCTCATCTTCTCTGA (SEQ ID NO: 296)

# **AOLFR162 sequences:**

15 MMRLMKEVVRGNQTEVTEFLLGLSDNPDLQGVLFALFLLIYMANMVGNLGMIVLIKIDLCLH  
 TPMYFFLSLSEFVDASYSSSVTPKMLVNLMAENKAISFHGCAAQFYFFGFLGTCEFLLAMMA  
 YDRYAAIWNPLLXPVLVSGRICLLIATSFLAGCGNAAIHGTMLFRSLFCGSGNRNHFYCDTPPL  
 LKLSCSDTHFNIGMAESSFVISCVMIVLISYLCLFI AVLKMPSLGRHKAFSTCSYLMVPTIF  
 FGTILFMYLRPTSSYSMEQDKVVSVFYTVIIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID  
 20 NO: 297)  
 ATGATGAGACTTATGAAAGAGGTTCTGAGGCAGAAATCAAACAGAAGTAACAGAATTTCTC  
 CTCTTAGGACTTCCGACAATCCAGATCTACAAGGAGTCTCTTTGCACTGTGTTCTGTTGAT  
 CTATATGGCAAACTGTGGGCAATTTGGGAGTGATTGTATTGAATGAAGATTGATCTGTG  
 25 CTCCACACCCCCATGTATTTCTTCTCAGTAGCCCTCTCTTTGTAGATGCCCTTACTCTTCT  
 TCCGCTACCTCCCAAGATGCTGGTGAACCTCATGGCTGAGAAATAAGGCCATTTCTTTTCATG  
 GATGTGCTGCCAGTTCTACTTCTTTGGCTCCTCTCTGGGAGCTGAGTGCTTCTCGTTGGCC  
 ATGATGGCATATGACCCTATGCAGCCATTGGAACCCCTGCTCATCCAGATTCTCGTGT  
 CTGGGAGAAATTGCTTTTGTCTAATAGCTACCTCCTTCTTAGCAGTTGTGGAAATGCAGC  
 30 CATACATACAGGGAATGACTTTTAGTTGTCTTTTGTGGTTCTAATAAGGATCAACCATTTCT  
 ACTGTGACACCCGCCCATCTCTCAAACTCTCTTGTCTGATACCACTCAATGGCATTTGTG  
 ATCATGGCATTCTCAAGTTTATTTGTATCAGCTGTGTTATGATTGTCTCATTTCCTACCT  
 GTGTATCTTCAATTGCGGTCTTGAAGATGCCTTCGTAGAGGGCAGGCACAAAGCCTCTCC  
 ACCTGTGCCTCTTACCTCATGGCTGTACCATATTCTTGAACAATCTCTCTCATGTACIT  
 35 GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTGTCTTTTATATACAGTA  
 ATAATCCCTGTGCTAAATCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAGGCC  
 TAAAGAAGATCTTATGGAAACACATCTTGTAG (SEQ ID NO: 298)

# **AOLFR163 sequences:**

40 MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVSLTVVGNSTLVLICNDSCLHTPMYFFTGN  
 LSLFLDWYSSVYTPKLVTCISEDKSIISFAGCLCQFFFSAGLAYSECYLLAAVAYDRVYAIKPL  
 LYAQAMSKILCALLVAVSYCGGFINSIITKTFNFCRENIIDDFCDLLPLVSELACGEKGGYK  
 IMMYFLASNVICPAVLYLASYLFIITSVLRISSSKGYLKAFTSCSHLTSVTLYLSGSIYIALPRS  
 SYSFDMDKIVSYFYTVVPPMLNMIYSLRNKDVKALKKLLP (SEQ ID NO: 299)  
 45 ATGCAGAGGAGCAATCATACAGTGACTGAGTTTATACTGCTGGGCTTACCACAGACCCA  
 GGAATGCAGCTGGGCTCTTCTGGTGTCTCTGGGCGTGTACTCTCTCACTGTGGTAGGAA  
 ATAGACCCCTCATCGTGTGTGATCTGTAATGACTCCTGCCTCCACACCCCATGTATTTTTC  
 ACTGGAAATCTGTGCTTTCTGGATCTCTGGTATTCTTCTGTACACACCCCAAGATCCTAGT  
 50 GACCTGACATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCGTGTGTCAGTTCTTCTCT  
 CTGCAAGGCTGCCATATAGTGAGTGCTACCTGCTGGCTGCCGTATGACCGCTACGT  
 GGCCATCTCCAAGCCCTGTCTTATGCCAGGCCATGTCCAATAAGCGTGTGTCATGTGCTG  
 GTAGCAGTCTCATATTGTGGTGGCTTTATTAATCTTCAATCATCAACCAAGAAACGTTTTCT  
 CTTAACTCTGCCGTGAAAAACATCATGTGACTTTTCTGTGATTGCTTCCCTTGGTGA  
 55 AGTGCGCTGTGGCGGAGAAAGGCGGGCTATAAAATATGATGTACTCTCTGCGGCCCTCA  
 GTCTACTGCCCGCAGTGCTCATCTGGCTCCTCACTCTTATATCATACAGGATGCTTGA  
 GGATCTCTCTCCAAGGGCTACCTCAAAGCCTTCTCCACATGCTCTCCCACTGACCTCT

GTCACITTTATACTATGGCTCCATTCTCTACATCTACGCTCTCCCCAGATCTAGCTATTCTTT  
TGATATGGACAAAATAAGTTTCTACATTTTACACTGTGGTATTCCCCATGTTGAATCTCATG  
ATCTACAGCCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAAACTTCTCCCATAA (SEQ  
ID NO: 300)

5

**AOLFR164 sequences:**

MFLTERNTTSEATFTLLGFS DYLELQIPLFFVFLAVYGFSSVGNLGMVVIKINPKLHPMYFFLN  
HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGCLVQFFFFCTFVVTELILFAVMAYDHFVAICNP  
LLYTVIAISQKLCAMLVVVLYAWGVACSLTLACALKLSFHGFNTINHHFCELSSLSISYPDSYL  
SQLLFTVTATFNEISTLLILTSYAFIIVTTLKMP SASGHRKVFS TCASHLTAITFIHGTLILFYCP  
NSKNSRHTVKVASVFYTVVPLNLPLIYSLRNKDVKDAIRKIINTKYFHIKHRHWYPNFVIEQ  
(SEQ ID NO: 301)

10

ATGTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTTACTCTCTTGGGCTTCTCAG  
ATTACCTGGAAC TGCAAATCCCCTCTCTTGTATTCTGGCAGCTACGGCTTCAGTGTG  
GTAGGGAATCTTGGGATGATAGTGATCATCAAAATTAACCCCAAAATTTGCATACCCCATGT  
ATTTTTCCTCAACCACTCTCCTTTGTGGATTCTGCTATTCTCCATCATTTGCTCCCATGA  
TGCCTGTGTAACCTGGTGTGAAGAAGATAAGACCATTTCTCTCAGGATGTTTGGTGCAATT  
CTTTTCTCTTTGACCTTTGTAGTGACTGAATTAATTCTATTGCGGTGATGGCCTATGACC  
ACTTTGGGCCATTTGCAATCCTCTGCTCTACACAGTTGCCATCTCCAGAAACTCTGTGCC  
ATGCTGGTGGTGTATTGTATGTCATGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCTG  
CTTTAAAGTTATCTTTTCATGGTTTCAACACAATCAATCATTTCTCTGTGAGTTATCCCTC  
CTGATGACTCTCTTACCCTGACTCTTATCTCAGCCAGTTGCTCTTTTCACTGTGGCCAC  
TTTAAATGAGATAAGCACACTACTCATCTTCTGACATCTTATGCAATTCATCAITTTGCACCA  
CCTTGAAGATGGCTCTCAGCCAGTGGGCACCGCAAAGTCTTCTCCACTGTGCCCTCCCACT  
GACTGCCATCACCATCTTCCATGGCACCATCTCTTCTCTACTGTGTACCAACCTCCAAAC  
ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCTTGTGAA  
TCCCTGTACTACAGTCTGAGAAATAAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT  
ACAAAATATTTTTCATATTAACATAGGCATTGGTATCCATTTAATTTTGTATTGAACAATA  
A (SEQ ID NO: 302)

30

**AOLFR165 sequences:**

MAVGRNNTIVTKFILLGLSDHPQMKIFL FMLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL  
SNLSFLDICVYSSTAPKMLS DIITEQKTSIFVGCAQTQYVFVFCGMLTECFLLAAMAYDRYAIAICN  
PLLYTVLISHILCLKMVVGYAVVGGFLSSFIETYSVYQHDFCGPYMINHFFCDLPPVLA LSCSDTF  
TSEVVT FIVSVVVGIVSVLVVLISYGYIVA AVVKISSATGRTKAFSTCASHLTA VTLFYGSGFFM  
YMRPSSSYSLNRDKVVSIFYALVIPVVPNIYSFRNKEIKNAMRKAMERDPGISHGPGPFIMTLG  
(SEQ ID NO: 303)

35

ATGGCTGTAGGAAGGAACAACAATTGTGACAAAAATCATTTCTCCTGGGACTTTGACAGC  
ATCTCAAAATGAAGATTTTCTCTTTTCATGTTATTTCTGGGGCTCTACCTCTGACGTTGGCC  
TGGAACTTAAGCCCTCATTGCGCCTATTAAGATGGACTCTCACCTGCACATGCCCATGTA  
CTCTCTCAGTAACTGTCTCTCTGGACATCTGCTATGTGCTCTCAACCGCCCTCAAGATG  
CTGTCTGACATCATCAGAGCAGAGAAACCAATTTCTTTGTTGGCTGTGCCATCAGTACT  
TTGCTCTCTGTGGGATGGGGCTGACTGAATGCTTTCTCTCGGACGATGTGGCCTATGACCG  
GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCTCATATCCCATACACTTTGTTTAA  
AGATGGTGGTGTGGCGCCTATGTGGGTGGATTCCTTAGTTCTTTTCATTGAACACATACTCTGT  
CTATCAGCATGATTCTCTGTGGGCCCTATATGATCAACCACTTTTCTGTGACCTCCCTCCAG  
TCTCGCTCTGCTGCTGCTGATACCTTCAACGAGCGAGGTGGTGACCTTCATAGTCAGTGGT  
TGTGTTGGAATAGTGCTGTGCTAGTGGTCTCATCTTATGGTATACATTTGCTGCTGT  
TGTGAAGATGACCTCAGCTCAGGTAGGACAAAGGCCCTCAGCATTTGTGCTCTCACTG  
ACTCGTGACACCTCTTCTATGGTCTGGATTCTTCATGACATGCGACCCAGTTCACGTA  
CTCCCTAAACAGGGACAAGGTGGTGTCCATATTTCTATGCCTTGGTGATCCCCGTGGTGAAT  
CCCATCATCTACAGTTTATAGGAATAAGGAGATTA AAAAATGCCATGAGGAAAGCCATGGAA  
AGGAGCCCGGGATTCTCACGGTGGACCATTCATTTTATGACCTTGGGCTAA (SEQ ID  
NO: 304)

55

**AOLFR166 sequences:**

MEMENCTRVKEFIFLGLQTNREVSLLVFLFLLLVYVTTLLGNLLIMVTVTCESRLHTPMYFLLH  
5 NLSIADICFSSITVPKVLVDLLSERKTISFNHCFQTMFLFHLIGGVDFVSLVSMALDRYVAISKPL  
HYATIMSRDHCIGLTVAAWLGGFVHSIVQISLLPLPFCGPNVLDTFYCDVHRVLKLAHTDIFIL  
ELLIMISNNGLLTTLWFFLLVSYVIVLSLPSQAGEGRRAKISTCTSHITVTVLHFVPCIVVYARP  
FTALPMDKAISVTFTVISPLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

10 ATGGAGATGGAAAAGCTGCACCAGGGTAAAAGAAATTTATTTTCCTTGGCCTGACCCAGAATC  
GGGAAGTGGAGCTTAGTCTTATTTCTTTTCTTACTCTTGGTGTATGTGACAACCTTTGCTGGGA  
AACTCTCTCATGTGCTACTGTTACTGTGAATCTCGCTTACACGCCCATGATATTTT  
GCTCCATAATTTATCTATTGCCGATATCTGCTTCTTCCATCACAGTGCCCAAGGTTCTGG  
TGGACCTTCTGCTGAAAGAAAAGACCATCTCCTCAATCATTGCTTCACTCAGATGTTCTTA  
15 TTCCACCTTATTGGAGGGGTGGATGTATTCTCTTTTCGGTGATGGCATTGGATCGATATG  
TGGCCATCTCCAAGCCCCTGCACATATGCGACTATCATGAGTAGAGACCATTGCAATGGGCT  
CACAGTGGCTGCTGCTGTTGGGGGGCTTTGTCCACTCCATCGTGACAGATTTCCTGTTGCTC  
CCACTCCCTTTCTGCGGACCCAAATGTTCTTGACACTTTCTACTGTGATGTCCACCGGGTCT  
CAAACCTGGCCCATACAGACATTTTCATACTTGAACATAATGATTTCCAACAATGGACTG  
20 CTCACCACTGTGGTTTCTGCTGCTGCTGCTGCTACATAGTCATATTATCATATACCCAA  
GTCTCAGGACGAGAGAGGAGGAGGAGGAAAGCCATCTCCACTGCACTCCCACTCAGTGT  
GGTGACCTGCATTTCTGCGCCCTGCATCTATGCTATGCCCGGCCCTTCACTGCGCTCCCCA  
TGATAGAGGCATCTCTGTCACCTTCACTGTCATCTCCCTCTGCTCAACCCCTGATCTAC  
ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCCT  
25 TCTGATAGAAAATAG \*SEQ ID NO: 306)

**AOLFR167 sequences:**

MSITKAWNSSSVTMFILLGFTDHPHELQALLFVTFGLIYLLTALWNLALIFLRGDTLHHTPMYFF  
LSNLSFIDICYSsavAPNMLTDFFWEQKTSIFVGCAGAAQFFFFVGMGLSECLLLTAMAYDRYAAI  
30 SSPLYPTIMTQGLCTRGMVVYAYVGGFLSSLQASSIFRLHFCGPNINHHFCDLPPVLALSXSDDT  
FLSQVNVLLVVVTVTGMVSFLQLLISYGYIVSAVLKPSAEGRWKASHLCASHLMVTVLLGTAL  
FVYLRPSSSYLLGRDKVVSFVSYSLVIPMLNPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID  
NO: 307)

35 ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTTCATCCTCTGGGATTCA  
CAGACCCTCAGAACTCCAGGCCCTCCTCTTTGTGACCTTCTCGGGCATCTATCTTACCACC  
CTGGCCTGGAACCTGGCCCTCATTTTCTGATCAGAGGTGACACCCATCTGCACACACCCA  
TGTACTTCTTCTCAAGCAACTTATCTTTTCATGTGACATCTGCTACTCTTCTGTGTGGCTCCC  
AATATGCTCATGACTTCTTCTGGGAGCAGAAGACCATATCATTTTGTGGCTGTGCTGCTC  
40 AGTTTTTTTTCTTTGTGCGCATGGGTCTGCTGAGTGCCTCCTCTGACTGCTATGGCATA  
GACCGATATGACGCCATCTCCAGCCCCCTTCTACCCCACTATCATGACCCAGGCGCTCT  
GTACACGCATGGTGGTGGGGCATATGTTGGTGGCTTCTGAGCTCCCTGATCCAGGCCAG  
CTCCATATTTAGGCTCACTTTTGGGACCCAAACATCAACCACTTCTTCTGGGAGCTCC  
CACCAGTCTGGCTCTGTCTTGTCTGACACCTTCTCAGTCAAGTGGTGAATTTCTCTGTG  
50 GTGGTCACTGTGCGGAGGAACATCGTTCTCCAACTCCTTATCTCCTATGGTTACATAGTGT  
CTCGGCTCTGAGAGATCCCTCAGCAGAGGGCCGATGGAAGCCCTGCAACACGCTGTGCTCT  
CGCATCTGATGGTGGTGACTCTGCTGTTTGGGACAGCCCTTTCTGCTGACTTGCAGCCAG  
CTCCAGCACTTGTCTAGGACAGGACAAAGGTGGTGTCTGTTTCTATTCACTGGTGAATCCCC  
ATGCTGAACCCCTCTCATTTACAGTTTGAAGAACAAAGAGATCAAGGATGCCCTGTGGAAG  
60 GTGTTGGAAAGGAAGAAAGTGTCTTCTTAG (SEQ ID NO: 308)

**AOLFR168 sequences:**

MEKINNVTETFIWGLSQSPEIEKVCFVVSFFYIIILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV  
DICTSSVTAPKIMVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAYDRYVAICKPLHYM  
70 TIMNRETCKNMLLGTWVGGFLHSIIQVALVVQLPFCGPNEDHYFCDVHPVLKLACTETIYVG  
VVVTANSGLTALGSFVILLISYIIIVSLRKQSAEGRRKALSTCGSHIAMVVIFGPGCTFMYMRPD



TTFSEDKMVAVFYTHITPMLNPLIYTLRNAEVDKAMKKLWGRNVFLEAKGK (SEQ ID NO: 309)

5 ATGGAAGAAAAATAAACACGTAACAGTAATTCATTTTCTGGGGTCTTTCTCAGAGCCCAAGAGAG  
TTGAGAAAGTTGTTTGTGGTGTGTTCTTCTCTCATATAATCATCTTCTCGGGAATCTC  
CTCATCATGCTGACAGTTTGCCTGAGCAACCTGTTTAAAGTCACCCATGTATTCTTCTCAG  
CTTCTTGCTCTTTGTGGACATTGTGTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC  
10 TGTTAGCAAAAGGACAAAACCATCTCTTATGTGGGGTGTCATGTGCAACTGCTTGGAGTAC  
ATTCTCTTGGTGTGACTGAGATCTTCATCTTACTGTAATGGCCCTATGATCGTTATGTGGCT  
ATCTGTAAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT  
TAGGGACCTGGGGTAGGTGGGTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCCAACT  
ACCCCTTGTGGACCAATGAGATAGATCACTACTTTGTGATGTTACCCCTGTGTTGAAAC  
CTTGCCTGCACAGAAACATACATTGTGTGGTGTGTTGTGACAGCCAACAGTGGTACCATTG  
CTCTGGGGAGTTTGTGTTATCTTGCTAATCTCTACAGCATCATCTAGTTTCCCTGAGAAAG  
15 CAGCAGCAGAAAGGAGCGCAAGCCCTCTCCACTGTGGCTCCCACTGGCATGCGATGGTCTG  
TTATCTTTTTTCGGCCCTGTACTTTATGTACATGCGCCCTGATACGACCTTTTCAGAGGAT  
AAGATGGTGGCTGTATTTTACACCAATTATCACTCCCATGTTAAATCTCTGTTTATACACT  
GAGAAATGCAGAAAGTAAAGAAATGCAATGAAGAAACTGTGGGGCAGAAATGTTTCTTGGA  
GGCTAAAGGGAATAG (SEQ ID NO: 310)

20

**AOLFR169 sequences:**

MMDNHSSATEFHLLGPPGSQGLHHILFAIFFFFYLVTLMGNTVIIVIVCVDKRLQSPMYFFLSHL  
STLEILVTTHVPMMLWGLFLGCRQYLSLHVSLSNFCGTMFEFALLGVMAVDRYVAVCNPLRY  
NIMNSSTCIWVVVSVVWVFGLEIWIPIATQFTRKNSLNDHFYCDRGQLKLSCDNTLLTEFI  
25 LFLMAVFIILGSLPIVSVYTHIISTILKIPASGRKAFSTFASHFTCVVIGVYGSCLFLYVKGPKQTQ  
GVEYNKIVSLLSVLTPLNPFIFTLRNDKVKALRDMKRCCQLLKD (SEQ ID NO: 311)

ATGATGGACAACCACTCTAGTGCCACTGAATTCACCTTCTAGGCTTCCCTGGGTCCCAAG  
GACTACACCAACATTTCTTTGCTATATTCTTTCTCTATTAGTGACATTAATGGGAAGAC  
30 ACGGTTCATCTGTTGATTGCTGTGAGGATAAAGCTGTGACATGCCCATGTTCTTCTCT  
CAGCCACTCTCTACCTCGGAGATCTCGGTCAACACATAATGTCCCATGATGCTTTGG  
GGATTGCTCTCTCTGGGATGACAGACGATCTTCTCTACATGATTCGCTCAACTTTTCTGT  
TGGGACCATGGAGTTTGCAATTACTTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTG  
AATCCCTTTGAGGTACAACATCATTAAGAACAGCAGTACCTGTATTGGGTGGTAATAGTGT  
35 CATGGGTGTGTTGGATTCTTCTGAAATCTGGCCCATCTATGCCACATTCAGTTACCTTC  
CGCAATCAAAATCATTAGACCATTTTACTGTGACCGAGGGCAATGTCTCAAACTGTCT  
CGCATAACTCTCTCACAGAGTTTATCTTTCTTAAATGGCTGTTTATTTCTTCAATGGT  
TCTTTGATCCCTACGATTGTCTCTACACCTACATTATCTCCACCATCTCAAGATCCCGTC  
AGCTCTCTGGCCGGAGGAAGGCCCTCTCCACTTTTGGCTCCCACTCAGCTGTGTGTGATTG  
40 GCTATGGCAGCATCTGTGTTCTCTACGTGAAACCCCAAGCAACACAGGGAGTGTGAGTACAA  
TAAGATAGTTTCCCTGTGTGTTCTGTGTAAACCCCTCTCTGAACTCTTTCATCTTTACTCT  
TCGGAATGACAAAGTCAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCTCT  
GAAAGATTAG (SEQ ID NO: 312)

45 **AOLFR170 sequences:**

MSFTSLIPSLCFSLTPLFLFCYLSLLPFLSAFLFTRWLLAFLSLFSVSVVSVSSVSSMVLCLYLSVS  
ASPSVFCFSCMQPILWIMANLSQPSFVLLGSSFGELQALLYGPGMLYLLAFMGNTHIIVMVI  
ADTHLHNPMYFFLGNFSLLEILVTMTAVPRMLDLHLVPHKVIITFGCMVQFYHFHSLGTSFLIL  
TDMALDRFVAICHPLRYGTLMSRAMCQVLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVINH  
50 FDCNEPLLQLSCSDTRLLEFWDLFMALTFVLSSFLVTLISYGVIVTTLRIPASSCCQKAFSTCG  
SHLTLVFIGYSSTIFLYVVRPGKAHSVQVRKVVALVTSVLTPLNPFILTFNCQTVKTVLQGGMQ  
RLKGLCKAQ (SEQ ID NO: 313)

ATGTCCTTCACTTCTCTACACCTCACTCTGTTTCTCTTGACTCTCCCATCTCTGTTTGT  
TATCTTCTTATTGCCGTTCTTCTGCTTCTTCTGTTATCACTGCTGGCTACTGCTTCT  
CTCTCTATTCTCTGCTCTGCTCTGTTTCTTCTGTTTCAAGTTCAATGGTCTCTGCTCTC

TATCTCTCTGTTTCTGCCTCTCCGCTCTGCTTTTGTCTCTTGTCATGCAGGGCCCCACTG  
 TGGATCATGGCAAATCTGAGCCAGCCCTCGAAATTTGTCTCTTGGGCTTCTCCTCTTGG  
 TGAGCTGACGGCCCTCTGTATGAGCCCTTCTCTCATGCTTTATCTTCTCGCCTTCATGGGAA  
 ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCATGACTTCTTC  
 5 TCGGGCAATTTTCCCTGCTGGAGATCTTGGTAACCATGACGTGCAAGTGGCCAGGATGCTCT  
 CAGACCTGTTGGTCCCCACAAAGTCATTACCTTCACTGGCTGCAATGGTCCAGTTCTACTTCT  
 CACTTTTCCCTGGGGTCCACCTCCTTCTCTGACAGACATGGCCCTGCTGCGCTTTGT  
 GGCCATCTGCCACCCACGCTGCGCTATGGCACTCTGATGAGCCGGGCTATGTGTGCCAGCTG  
 GCTGGGGCTGCTGGGAGCTCCTTTCTAGCCATGGTACCCAATGCTCTCTCCCGAGCTG  
 10 ATCTTGATTACTGCCATGGCGACGTCATCAACCACTTCTTCTGTGACAATGAACCTTCTCCTG  
 CAGTTGTGATGCTCTGACACTCGCCTGTTGGAATTTCTGGGCAATTTCTGATGGCCTTGACCTT  
 TGTCTCAGCTCCTTCTGCTGGTGAACCTCATCTCTATGCTACATAGTGACCATGTGCTGCG  
 GGAATCCCTCTGCCAGCAGCTGCCAGAAGGCTTTCTCCACTTGGCGGCTCACTCTCACACT  
 GGTCTTCATCGGCTACAGTAGTACCATCTTTCTGTATGTGAGGCGTGGCAAAGCTCACTCT  
 15 TTACCAAGTCAGGAAGTCGTGGCCTTGGTGACTTCACTTCTACCCCTTCTTCAATCCCT  
 TTATCCTTACCTTGTGCAATCAGACAGTTAAACAGTGTACAGGGGCAGATGCAGAGGCT  
 GAAAGGCTTTGCAAGGCACAAATGA (SEQ ID NO: 314)

**AOLFR171 sequences:**

20 MVGNLIWVTTIGSPSLGSLMYFFLAYLSLMDAIYSTAMSPKLMIDLCKIAISLSACMGQLFI  
 EHLHGGAEVFLLVVMAFYDRYVAISKPLHYLNIMNRLVCILLVVAMIGGFVSVVQIVFLYSLP  
 ICGPNVIDHSDVMYPLLELLCLDTYFGLTVVANGGHCMIPTFLLISCGVILNFKLTYSQER  
 HKALPTCISHIIVVALVFVPCIFMYVRPVSNNPFDKLMTVFYSIITLMLNPLIYSLRQSEMKNAM  
 25 KNLWCEKLSIVRKRVSPILNIFPSSKATNRR (SEQ ID NO: 315)

ATGGTGGGAAACCTCCTCATTTGGGTGACTACTATTGGCAGCCCTCCTTGGGCTCCCTAA  
 TGTACTTCTCCTTGTGCTTGTCACTTATGGAATGCCATATATCTCACTGCCATGTGCAACC  
 AAAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTTCTTGTGAGCTTGCATGGGTC  
 AGCTCTTCATAGAAACACTTACTTGGTGGTGCAGAGGCTCTTCTTTTGGTGGTGTAGGGCTA  
 30 TGATCGCTATGTGGCTATCTCTAAGCCGCTGCACTATTGGAACATCATGAATCGACTGGTT  
 TGATCCTTCTGTGTGGTGGTGGCCATGATGGAAGGTTTGTGCACTCTGTGGTTCAAATTTGT  
 CTTTCTGTACAGTCTACCAATCTGTGGCCCAATGTTATTGACCACTCTGTCTGTGACATGT  
 ACCCATTTGTGGAATGTTGTGCTTGAACCTACTTTATAGGACTCACTGTGGTTGGCCAA  
 TGGTGGAAATAATTGTATGGTCATCTTTACCTTCTGCTAATCTCCTGTGGAATCATCTCAA  
 35 ACTTCTTAAAACTTACAGTCAGGAAGAGAGGCATAAAGCCCTGCCTACCTGCATCTCCCA  
 CATCATTTGTGGTTGCCTCGTTTGTGTCCCTGTATTTTATGTATGTTAGACCCGTTTCCA  
 ACTTTCCCTTTGATAAAATTAATGACTGTGTTTATTCAATATACACACTCATGTTGAATCCT  
 TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGTGAA  
 AAGTTAAGTATAGTTTGA AAAAGAGTATCTCCACACTGAACATATTTATCTAGTTCTTA  
 40 AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)

**AOLFR172 sequences:**

MAETLQNLSTFLHPNFFILGTGPGLSAQTWLTLVFGPIYLLALLGNGALPAVVWIDSTLHQPM  
 FLLLAALATDLGLATSIAPGLLAVLWLGPRSVPYAVCLVQMFVHALTAMESGVLLAMACDR  
 45 AAAIGRPLHYPPVLVTKACVGYAALALALKAIVVPPFLVAKFEHFQAKTIGHTYCAHMAV  
 VELVVGNTQATNLVYGLALSISGMDILGITGYSGLIAHAVLQLPTREAHAKAFGTSCSHICVIL  
 AFYIPGLFSYLHFGHHTVPKPVHILLNLIYLLPPALNPLIYGARTKQIRDRLLFTTFRKSPL  
 (SEQ ID NO: 317)

50 ATGGCAGAACTCTACAACCTCAATTCCACCTTCTACACCCAACTTCTTCATACTGACTG  
 GCTTCCAGGGCTAGGAAGTGCCAGACTTGGCTGACACTGGTCTTTGGGCCCACTTATCT  
 GCTGGCCCTGCTGGGCAATGGAGCACTGCCGCGAGTGGTGTGATAGACTCCACCTGCA  
 CCAGCCCATGTTTCTACTGTGGCCATCTGGCAGCCACAGACCTGGGCTTAGCCACATCT  
 ATAGCCCCAGGGTGTGGCTGTGCTGTGGCTTGGGCCCGGACTGTCGGCATATGCTGTGT  
 55 CGCTGGTCCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTGGC  
 CATGGCTGTGATCGTGCTGCGGCAATAGGGCGTCCACTGCACCTACCTGTCTGTGTCACC

AAAGCCTGTGTGGGTATATGCAGCCTTGGCCCTGGCACTGAAAGCTGTGGCTATGTGTGTAC  
CTTTCCCACTGCTGGTGGCAAAAGTTTGAACACTTCCAAGCCAAAGACCATAGGCCATACCTGA  
TTGTGCACACATGGCAGTGGTAGAACTGGTGGTGGGTAACACAGGCCACCAACTTATA  
5 TGGTCTGGCACTTTCAGTGGCCATCTCAGGATATGGATATCTGGGTATCACTGGCTCCTAT  
GGACTCAATTGCCACTGCTGTGCTGCAGCTACCTACCCGGAGGCCATGCCAAAGGCTTTG  
GTACATGTAGTTCTACATCTGTGTCAATTCTGGCCCTCTACATACCTGGTCTCTTCTCTCTAC  
CTCGCACACCGCTTTGGTCAACACTGTCCCAAAGCCTGTGCACATCCTCTCTCCAAACAT  
CTACTTGTCTGTGCCACCTGCCCTCAACCCCTCATCTATGGGGCCCGCACCAAGCAGATC  
10 AGAGACCGACTCCTGGAACCTTCACATTGAAAAAGCCCGTTGTAA (SEQ ID NO: 318)

**AOLFR173 sequences:**

MSHTNVTIFHPAVFVLPPIGLEAYHIWLSIPLCLIIYITAVLGNLSILVIVMERNLHVPMYFFLS  
MLAVMDILLSTTTPKALAIFWLQAHNIAFDACVTQGFVHMMFVGESAILLAMAFDRFVAIC  
APLRYTTVLTPVVGRIALAVITRSFIIFVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV  
15 NIWYGSFVPIVMVILDVILLAVSYSILRAVFLRPSQDARHKALSTCGSHLCVILMFYVPSFTLL  
THHFGRNIPQHVHILLANLYAVPPMLNPVIVGVKTKQIREGVAHRFDIKTWCCSTPLGS  
(SEQ ID NO: 319)

ATGAGTCACACCAATGTTACCATCTTCCATCTGCAAGTTTTTGCTCTTCCGGCATCCCTGG  
20 TTGGAGGCTTATCACTATTGGCTGTCAATACCTCTTGGCCTCATTTACATCACTGTCAGTCC  
GTGGAAACAGCATCCTGATAGTGGTTATTGTCATGGAACGTAACCTTCATGTGCCCATGTIA  
TTTCTTCTCTCAATTGGCTGGCCGTATGGACATCTGCTGTCTACCCACCACTGTGGCCAAAG  
CCCTAGCCATCTTTGGCTTCAAGCACATAACATTCCTTTTGTAGCCTGTGTACCCCAAGCG  
25 TCTTTGTCCATATGATGTTTGTGGGGGAGTCAGCTATCCTGTTAGCCATGGCTTTTGTATCG  
CTTTTGGCCCAATTGTGGCCCACTGAGATATACAAACAGTGTCTAACATGGCCTGTGTGGGG  
AGGATTGCTCTGGCCGTATCACCCGAAGCTTCTGCATCATCTTCCAGTCAATATCTTGCT  
GAAGCGCTGCCCTTCTGCTCAACCAACATTTGCTCTCACTCTGAGCATATTGGGA  
GTGGCTCGTTAGCCTGTGCTGACATCACTGTTAAACATTTGGTATGGCTTCTCAGTGCCCAT  
30 TGTCAATGGTATCTTGGATGTTATCTCATCGCTGTGTCTTACTCACTGATCCTCCGAGCAG  
TGTTTCGTTTGGCTCCAGGATGCTCGGCACAAAGCCCTCAGCACTTGTGGCTCCCACT  
CTGTGTCATCCTTATGTTTTATGTCCATCCTCTCTTACCTTATTGACCCATCAITTTGGGCG  
TAATATTCCTCAACATGTCCATATCTTGTCTGGCCAACTTTATGTGGCAGTGACCCCAATGC  
TGAACCCCATTTGCTATGTTGTGAAGACTAAGCAGATACGTGAGGGGTGAGCCACCGGT  
35 CTTTGACATCAAGACTTGGTGTGTACCTCCCTCTGGGCTCATGA (SEQ ID NO: 320)

**AOLFR175 sequences:**

MHFLSQNDLNLNLIPLHCLHRHSVIAGAFTHRHMKIENSPSNSSTFTGFILLGFPCPREGQILLFV  
LFTVVYLLTLMGNSGICAVHWDQRLHAPMYILLANFSLEICYVTSVPSMLANFLSDTKIISF  
SGCFLQFYFFSLDSTECFFLAVMAFDRYLAIKRLPYPTIMTRRLCTNLVNCWVLGFIWFLPI  
40 VNISQMSGCGRDIHFLCDPAPLLTLTKKGPVIELVFSVLSPLVPMFLFVIGSVYLVVRAVL  
RVPSAAGRRKAFSTCGSHLAVVSLFYGSVLVYMGSPSPSKNEAGKQKTVTLFYSVVTPLNPVI  
YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

ATGCATTTTCTTCCCAAAATGATTTAAATATAAACTGATTCCCATCTATGTTTGCACCG  
45 TCATTAGTAATTGCTGGTGCTTTTACAATTACAGGCACATGAAAATCTCAACAGCCGC  
AGCAACTCCAGCACTTCACTGGCTCATCTCTCTGGGCTTCCCTTGGCCCAAGGAGGGG  
AGATCCTCCTCTTTGTGCTCTTCACTGTGTGTTTACCTCCTGACCCCTCATGGGCAATGGTTCC  
ATACATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCCCATGTACATCTGCTCGCCA  
ACITCTCCTTCTTGGAGATATGTTATGTCACTCCACAGTCCCCAGCATGCTGGCCAACTTC  
50 CTCTGTGACCAACAGATCATCTCGTTCCTGGCTGCTTCTCCAGTCTACTTTTCTTCTCTG  
TTGGGCTCTACAGAATGCTTTTCTGGCAGTTATGGCATTGATCGATACCTTGGCATCTG  
TCGGCCTCTACGCTATCCAACCATATGACCAAGCATCTCTGTACCAATCTGTGGTCAAT  
GCTGGGTACTTGGTTTCACTGCTGTTCTTGATTCCTATCGTCAACATCTCCAAAGTGCTTCT  
TGTGGATCTAGGATTATGACCACTTCTATGTGACCCAGCTCCTCTCTAATCTCACTGTC  
55 CAAAAAAGGCTCTGTATAGAGCTTGTCTTTCTGTCTTAAGTCTTCAAGTCTGCTGTCTTATGC  
TCTTCTCTTCAATGTGGGGGTCTATGCTCTGGTGTGAGAGCTGTGTGAGGGGTCCCTTCA

GCAGCTGGGAGAAAGGCTTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTTCACTGT  
TCTACGGCTCAGTACTGGTCACTGATGGGAGGCCACCATCTAAGAATGAAGCTGGAAGC  
AGAAGACTGTGACTCTGTTTATTCTGTGTACCCCACTGCTTAACCTGTGATATATAGT  
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTGGGGAACATAA (SEQ ID NO:  
322)

# **AOLFR176 sequences:**

MFFIIHSLVTSVFLTALGPQNRMTMHFVTEFVLLGFHGQREMQSFFSFLVLYLLTLNGNAIVC  
AVKLDRLRLHTPMYILLGNFALEIWIYSSTVPNMVLNLSIKTISFSGCFLQFYFFSLGTTECF  
LSVMAYDRYLAICRPLHYPSIMTKGFCILVCVWVGGFLCYPVPVILISQLPFCGPNIDHLVCD  
PGPLFALACISAPSTELICYTFNSMIIFGPFLSILGSYTVIRAVLCIPSGAGRIKAESTCGSHLMV  
VLSFYGTLMVMYVSPSTSGNPAGMQKIITLVYTAMTPFLNPLIYSLRNKDKMDALKRVLGLTVS  
QN (SEQ ID NO: 323)

ATGTTCTTTTATTATTCATTCTTTGGTTACTTCTGTTTTTCTAACAGCTTTGGGACCCAGAA  
CAGAACCAATGCATTTTGTGACTGAGTTTGTCTCTGGGTTTCCATGGTCAAAGGGAGATG  
CAGAGCTGCTTCTCTCATTATCTCTGTTCTCTATCTCCTGACACTGTAGGGAATGGAGC  
TATTGTCTGTGACGTAAATGGACAGCGGCTCCACACACCCATGTACATCTCTCTGGGA  
AACTTTGCCTTTCTAGAGATCTGGTACATTTCTCCTCACTGTCCCAACATGCTAGTCAATAT  
CCTCTCTGAGATTAAACCATCTCCTTCTCTGGTGTCTCTGCTCAATCTATTCTTTTCTTTC  
ACTGGGTACAACAGAGTGTCTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC  
TGTCGTCCATTACACTACCCCTCCATCATGACTGGGAAGTCTGTATAATCTGGTCTGTGT  
ATGCTGGGTAGCGGATTTCTCTGCTATCCAGTCCCTATTGTCTTATCTCCCAACTCCCT  
TCTGTGGGCCAACATCATGTACCACTTGGTGTGTGACCCAGGCCAATTGTTTGCACGTGGC  
CTGCATCTCTGCTCTCCCTCCACTGAGCTTATCTGTTACACCTTCACTCGATGATTATCTTIG  
GGCCCTTCTCTCCATCTTGGGATCTTACACTTGGTGTATCAGAGCTGTGCTTGTATTCCCT  
TGCTGTGCTGGTCGAACTAAAGCTTTCTCCACATGTGGTCCCACTAATGGTGTGTCTC  
TATTCTATGGAACCTTATGGTGTATGTATGTAGGCCAACATCAGGGAACCCAGCAGTAAG  
GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTCTTAAATCCCTTATCTAT  
AGTCTCTGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCTGGGGTTAACAGTTAAG  
CAAACTGA (SEQ ID NO: 324)

# **AOLFR177 sequences:**

MSFFFVLLRPMNRSATHIVTEFILLGFPGCWKIQLFSLFLVIYVLLTLNGNAIYAVRCNPLIH  
TPMYFLDGNFALEIWIYSSTIPNMVLNLSKTKAISFGCFLQFYFFSLGTTECLFLAVMAYD  
RYLAICHLQYPAIMTVRFGKLVSCFWLIGFLGYPIPIFYISQLPFCGPNIDHFLCDMDPLMAL  
SCAPAPITECIFYTQSSLVLFFTSMYILRSYILLTAVFQVPSAAGRRKAFSTCGSHLVVVSIFYG  
TVMVMYVSPITYGPIITLLQKILTLVYSVTPLFNPLIYTLRNKDKMLALRNVLFGMRIRQNS  
(SEQ ID NO: 325)

ATGTTCTTTCTTTTGTAGACTTAAGACCCATGAACAGGTGACGAACACACATCGTGACAG  
AGTTTATCTCTCTGGGATCCCTGGTGTCTGGAAGATTGAGATTTTCTCTTCTCATTGTTT  
TTGGTGATTATGTCTTTGACCTTGTCTGGGAAATGGAGCCATCATCTATGCAGTGAGATGCA  
ACCCACTACTACACACCCCATGTACTTTCTGCTGGGAAATTTGCCTTCCTTGAGATCTGG  
TATGTGCTCTCACTAATCTCAACATGCTAGTCAACATTCTCTCCAAGCAACAGGCCATCTC  
ATTTTCTGGGTGCTTCTCTCCAGTGTCTATTTCTCTTCTCACTGGGAACAACATGAATGTCTC  
TTCTGGCAGTAAATGGCTTATGATCGATACCTGGCCATCTGCCACCCATGCAGTACCCCTGC  
CATCATGACTGTAAAGGTTCTGTGGTAAGCTGGTGTCTTTCTGTGTGGCTTATTGGATTCTCTG  
GATACCCCAATTCCTATTTTCTACATCTCCCACTCCCTTCTGTGGTCTTAATATCAATTGAT  
CACTTCTGTGTGACATGGACCCATTGATGGCTCTATCTGTCGCCAGCTCCCAATCACTG  
AATGATATTTCTATACTACAGCTCCCTTGTCTCTTTTCACTAGTATGTACATCTTCGA  
TCTATATCTGTACTAACAGCTGTTTTTCAAGTCCCTTCTGCAGCTGGTGGGAGAAAAG  
CCTTCTCTACCTGTGGTCTCATTTGGTGTGGTATCTTTTCTATGGGACAGTCAATGGTA  
ATGTATGTAAGTCTACATATGGGATCCCAACTTATTGCAAGAAGTCTCACACTGGTAT  
ATTCACTGAACGACTCTCTTTTAACTCTGTACTATCTTCGTAATAAGGACATGAAA

CTCGCTCTGAGAAATGTCCTGTTTGGAAATGAGAATTCGTCAAAATTCGTGA (SEQ ID NO: 326)

**AOLFR178 sequences:**

5 MVGANHSVVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNLSILLTVTSDPHLHSPMYFLL  
ANLSFIDLGVSSVTSPKMIYDLFRKHEVISFGGCIQIFFHIVIGGVEMVLLIAMAFDRYVAICKP  
LQYLTIMSPRMCMMFLVAAVVTGLIHSVVLVVFVNLPCGPNVSDSFYCDLPRFLKLACTDSY  
RLEFMVNTANSGFISLGSFFLIHSYVVIILTVLKHSSAGLSKALSTLSAHVSVVVLFFGPLIFVYTW  
PSPSTHLDKFLAIFDAVLTPVLNPIHYTFRN (SEQ ID NO: 327)

10 ATGGTTGGGGCAAATCACTCCGTGGTGTGACAGATTTGTGTTCTCTGGGACTACCAATTCCT  
GGGAGATCCGACTTCTCCTCCTTGTGTTCTCCTCCATGTTTACATGGCCAGTATGATGGGA  
AACTCTCTCATTTTGTCTCACTGTGACTTCTGACCCTCACTGGCACTCCCCATGTATTTTCT  
GTTAGCCAACTCTCCTTCATTGACCTGGGTGTTTCTCTGTCACTTCTCCCAAAATGATT  
15 ATGACCTGTTTCAGAAAACGAAAGTCATCTCCTTTGGAGGCTGCATCGCTCAAAATCTTCTT  
CATCCACGTCATTGGCGGTGTGGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATA  
GTGGCCATATGTAAGCCCTCCAGTACCTGACCAATTAGAGCCCAAGAAATGTGCATGTCT  
TCTTAGTGGCTGCCTGGGTGACCGGCTTATCCACTCTGTAGTTCAATTGGTTTITTAGTA  
AACTTGCCTTCTGTGGTCTAATGTATCGGACAGCTTTTACTGTGACCTTCTCGGTTTCAT  
20 AACAACCTTGCCTGCACAGACGCTACCGACTGGAGTTTCATGGTTACAGCCAACAGTGGAATC  
ATCTCTCTGGGCTCCTTCTTCATACTGATCATTTCTTATGTGGTTCATCAITTCACCTGTCT  
GAAACACTTTCAGCTGGTTATCCAAAGGCTCTGTCCACCTTTCAGCTCACGTCAGTG  
GTAGCTTTTGTCTTTGGTCTCTTGATTTTGTCTATACGTGGCCATCTCCCTCCACACCT  
GGATAAGTTTCTGGCCATCTTTGATGCAGTTCTCACTCCTGTTTAAATCCTATCATCTACA  
25 CATTCAGGAATTGA (SEQ ID NO: 328)

**AOLFR179 sequences:**

30 MNGMNHSVVSEFVFMGLTNSREIQLLLFFVSLLYFASMMGNLVIVFTVTMDAHLHSPMYFLL  
ANLSIDMAFCSITAPKMICDIFKKHKAISFRGCTQIFFSHALGGTEMVLLIAMAFDRYMAICKP  
LHYLTIMSPRMCYFLATSSHGLHSLVQLVVFVVDLPFCGPNIFDSFYCDLPRLLRLACTNQEL  
EFMVTVNSGLISVGSFVLLVISYIFILFTVWKHSSGLAKALSTLSAHVTVVILFFGPLMFFYTW  
PSPSTHLDKYLAIFDAFITPFLNPVYTFRNKDMKVMRRCLSRLAHFTKIL (SEQ ID NO: 329)

35 ATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTATGGGACTACCAACTCAC  
GGGAGATTGAGCTTCTACTTTTGTGTTCTCTTTGTTGTTCTACTTTGCGAGCATGATGGGA  
AACCTTGTCTATGTATTCAGTGAACCATGGATGCTCATCTGCACTCCCCCATGTATTTCT  
CCTGGCTAACCTCTCAATCATTGATATGGCATTGTTGCTCAATTACAGCCCCATAGATGATTT  
TGATATTTTCAAGAACACAAAGGCCATCTCCTTTCGGGAATGTATTACTCAAGTCTTCT  
40 TAGCCATGCTCTTTGGGGCACTGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATA  
ATGGCCATATGTAAACCTCTCCACTACCTGACCATCATGAGCCCAAGAAATGTGTCTATACT  
TTTAGCCACTTCTCTATCATATGGCCTTATCCACTCATTGGTCCAATTAGTTTITTTGGTA  
GATTACCTTTTGTGGTCTAATATCTTTGACAGTTTITACTGTGATCTCCCTCGGCTCCT  
CAGACTTGCCTGTACCAACCAAGAACTGGAGTTTCATGGTCAATGATAGTGGACTC  
ATTCTGTGGGCTCCTTTGTCTTGTGGTAATTTCTACATCTTCATTCTGTTCACCTGTTG  
45 GAAACATCTTCTGTGGTGTGACCAAGGCCCTCTACCTGTGACGTCACTGATGTG  
GTCATCTTGTCTTTGGGCCACTGATGTTTTTCTACACATGGCCTTCTCCACATCACACCT  
GGATAAATATCTGCTATTTTGTGATGCAATTATTACTCCTTTTCTGAATCCAGTTATCTACA  
CATTCAGGAACAAAGACATGAAAGTGGCAATGAGGAGACTGTGCACTGCTTTCGCGCATT  
TTACAAAGATTTGTAA (SEQ ID NO: 330)

50

**AOLFR180 sequences:**

55 MTNKMVIAIYIKNLNYFSFLIVQCLQPTMAIFNNTSSSNFLLTAFPGLECAHVWISIPVCLLYTI  
ALLGNSMIFLVITKRRRLHKPMYFVLSMLAAVDLCITITLPTVLGVLWFHAREISFKACFIQMF  
FVHAFSLESSVLVAMAFDRFVAICNPLNYATILTRDMVLVIGLVICIRPAVFLPLLVAINTVSF  
HGGHLSHPFCYHPEVIKYTYSKPWISSFWGLFLQLYLNGLTDVLFILFSYVLIILRTVLGIVARKK

QQKALSTCVCHICAVTIFYVPLISLSLAHRLFHSTPRVLCSTLANIYLLPVLNPIIYSLKTKTIR  
QAMFQLLQSKGSWGFNVRGLRGRWD (SEQ ID NO: 331)

5 ATGACTAATAAAATGTATGTATATATATAAAGAATCTTAATTTATTTTCTTCTCCATAGT  
TCAGTGTCTTCAACCAACCATGGCAATATTCAATAACACCACCTTGGCTTCTCCTCAAACCTCC  
TCCTCACTGCATTCCTCGGGCTGGAAATGTGCTCATGTCTGGATCTCCATCTCCAGTCTCGTGT  
CTCTACACCATTGCCCTCTGGGAAACAGTATGATCTTTCTTGTCATCACTAATGAAGCGGA  
GACTCCACAAACCATGTATTAATTTCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC  
10 ATTACGACCCTCCCACTGTGCTTGGTGTCTCTGCGTTTCATGCCCGGGAGATCAGCTTTAA  
AGCTTGTCTTCATCAAAATGTTCTTTGTGTCATGCTTCTCCTTGGTGGAGTCTCGGTGTGG  
TAGCCATGGCCTTTCAGCGCTTCTGCGGCTATCTGTAACCCACTGAACAGTACTGTCTATCCTC  
ACAGACAGGATGTGCTGGTGTATAGGGCTGGTCTATGTCATTAGCACTGAGCTTTCTGTAC  
TTCCCTTCTTGTAGCCATAAACACTGTGTCTTTTCATGGGGGTGTCAGAGCTTTCCCATCCA  
15 TTTTGCTACCAACCCAGAAAGTGATCAAATACACATATTCAAAACCTTGGATCAGCAGTTT  
GGGCACTGTTCTTCAGCTCACTGCTGAATGGCACTGAGTATTTGTTATCTTTTCTCTCTAT  
GTCTGATCTCCCGTACTGTTCTGGGCATTTGTGGCCCGAAAGAGCAACAAAAAGCTCTCA  
GCACTTGTGCTGTGTCACATCTGTGCACTGATCTTTCTATGTGCACTGATCAGCCTCTCT  
TTGGCACAACCGCTTCTCACTCCACCCCAAGGGTGTCTGTAGCACTTTGGCCAAATATTTA  
20 TCTGCTCTTACAGCTGTGCTGAACCTATCATTTACAGCTTGAAGACCAAGACAATCCGC  
CAGGCTATGTTCCAGCTGTCTCAATCCAAGGGTTCATGGGGTTTAAATGTGAGGGGTCTTA  
GGGGAAGATGGGATTGA (SEQ ID NO: 332)

**AOLFR181 sequences:**

25 MSVLNNSEVKLFLLLIGIPGLEHAHIWFSIPICLMYLLAIMGNCTILFIKTEPSLHEPMYFLAML  
AVSDMGLSLSSLPTMLRVFLFNAMGISPNACFAQEFHIGFTVMESVLLIMSLDRFLAIHNPLR  
YSSILTSNRVAKMGLILAIRSILLVIPFPFTLRLLKYVCQKNLSHSYCLHQDTMKLACSDNKTNV  
IFGFIALCTMLDLALIVLSYVLILKLTILSIASLAERLKAINTCVSHICAVLTFFVPITLAAHHF  
AKHKSPVLVILIADMFLLVPLMNPVIVCVKTRQIWEKILKLLNVCGR (SEQ ID NO: 333)

30 ATGTCTGTCTCAATAACTCCGAAGTCAAGCTTTTCTCTGATTGGGATCCCAGGACTGG  
AACATGCCACATTTGGTTCTCCATCCCCATTTGCCATGTAAGTCTTGGCATCATGGGGC  
AACTGCACCATTTCTTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATTT  
CCTTGCCATTTGGCTGTCTCTGACATGGGCGTGTCCCTCTCTCCCTTCACTAGCATGTTGA  
35 GGGTCTTCTTGTTCATGCCATGGGAATTTCACTAATGCCTGCTTTGCTCAAGAATCTTCT  
ATTCACTGATTCAGTGTGATGGAATCCTCAGTACTCTAATATATGCTTTGGACCGCTTTCT  
TGCCATTACAATCCCTTAAGATACAGTCTATCTCTCACTAGCAACAGGGTGTCTAAAATG  
GGACTTATTTAGCCATTAGGAGCATCTCTTAAGTATTCATTTCCCTCACCTTAAGGAG  
ATTAATAATATTGTCAAAAGAATCTTCTTCTCACTCATCTGTCTTCATCAGGATACCATGA  
AGCTGGGCTGTCTGACAACCAAGACCAATGTCATCTATGGCTCTTTCATGTCTCTGTACT  
40 ATGCTGGACTTTGGCAGTATGTTGTTTGTCTTATGTGCTGATCTTGAAGACTCATACTGACAT  
TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAATACCTGTGTCTCCACATCTGTGTCTGTG  
CTCACCTTCTATGTGCCATCATCACCCCTGGCTGCTCATCATCTTTGCCAAGACACAAA  
GCCCTCTTGTGTGATCCTTATGTCAGATATGTTCTGTGTGGTGCCGCCCTTATGAACCCC  
45 ATGTGTACTGTGTAAGACTCGACAATCTGGGAGAAGATCTTGGGAAGTTGCTTAAT  
GTATGTGGGAGATAA (SEQ ID NO: 334)

**AOLFR182 sequences:**

50 MTLGSLGNSSSVSATFLLSGIPGLERMHIWISIPCFMYLVSIPGNCTILFIKTERSLHEPMYFLFL  
SMLALIDLGLSLCTLPTVLGIFVVGAREISHDACFAQLFFHCFSESSVLLSMFDRFVAI  
LHYVSLTNTVIGRIGLVSLGRSVAILFPLPFMLKRFYVCGSPVLVSHSYCLHQVEMKLACADMK  
ANSIYGMFVIVSTVGIDSLILFSYALILRTVLSIASRAERFKAINTCVSHICAVLLFPTMIGLSV  
IHRFGKQAPHLVQVVMGFMYLLPPPVMNPVIVSVKTKQIRDRVTHAFY (SEQ ID NO: 335)

55 ATGACCCTGGGATCCCTGGGAAACAGCAGCAGCAGCTTCTGCTACCTTCTGCTGAGTG  
GCATCCCTGGGCTGGAGCGCATGCACATCTGGGATCTCCATCCCATGCTGCTCATGTCT  
GGTTTCCATCCCGGCAACTGCACAATCTTTTATCATTAATAACAGAGCGCTCACTTCAT

GAACCTATGTAATCTCTCTGTCATGCTGGCTCTGATTGACCTGGGTCTCTCCCTTTGCAC  
TCTCCCTACAGTCTGGGCATCTTTTGGGTGGAGCACGAGAAATTAGCCATGATGCTCTGC  
TTTGCTCAGCTCTTTTTCATTCACTGCTCTCTCTCGAGTCCCTCTGTGCTACTGTCTATG  
GCCTTTGACCGCTTTTGTGGCTATCTGCCACCCTTGCACTATGTTTCCATTCTACCAACAC  
AGTCATTGGCAGGATTTGGCCTGGTCTCTCTGGGTCTGATGTAGCACTCATTTTTCCATT  
5 CTTTATATGCTCAAAAGATTCCCTTATTGTGGCTCCCGAGTTCTCTCACATCTCTATTGTCT  
CCACCAAGAAGTGATGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCTACGGCAT  
GTTTGTCACTGCTCTACAGTGGGTATAGACTCACTGCTCATCCTCTCTCTATGCTCTGA  
10 TCGTGGCAGCGTGTGTCATCGCCTCCAGGGCTGAGAGATTCAAGGCCCTTAACACCTG  
TGTTTCCACATCTGTGCTGTGCTCTTCTACACTCCCATGATTGGCCTCTCTGTCACTCC  
ATCGCTTTGGAAAGCAGGCACCCACCTGGTCCAGGTGGTTCATGGGTTTCATGATCTTCT  
CTTCTCTCTGTGATCGAATCCCATGTCTACAGTGTGAAGACCAACAGATCCGGATCGA  
GTGACGCATGCCTTTTGTACTAA (SEQ ID NO: 336)

15 **AOLFR183 sequences:**

MTNLSNASQNHRTITGIPGTPDKNPWLAFLPLFLYTLTLLNGNTILAVIKVEPSLHEPTYFL  
SILALTDVLSMSLTSLMSLSIYWFNAPQIVFDACIMQMFHIVFGIVESGVLVSMADFRFVAIRN  
PLHYVSILTHDVIRKTGISVLTRAVCVVPVFLIKCLPFCHSNVLSHSYCLHQNMRLACASTR  
INSLYGLIVIFTLGLDVLTLTLLSYVLTLKTVLGIYSRGERLKTSLCLSHMSTVLVIFYVPMGA  
20 ASMIHRFWEHLSPVVHVMVADIYLLPPVLNPIVYSVKTKQI (SEQ ID NO: 337)

ATGACGAACTTGAATGCATCACAGGCCAACCCGTAACCTTCATTCTGACAGGTATCCCGAG  
GAACGCCAGACGAAGAACCCTATGGTTGGCTTTTCCCTGGGATTTTCTACACACTACACT  
25 CCTGGGAAATGGTACCATCTAGCTGTCACTCAAGGTGGAGCCAAAGTCTCCATGAGCCACG  
TATTAATCTCTTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGCCCTCC  
ATGCTCAGCATCTACTGGTTTAATGCCCTCAGATTGTTTGTATGCATGCATCATGACGAT  
GTTCTTCATCCATGTATTGGGAATAGTAGAATCAGGAGTCTAGTGTCCATGGCCTTTGAC  
AGATTTTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCTCACTCAGATGTTATTCTG  
30 AAAGACTGGAATATCTGTCCTCACCCGGGAGCTGTGTGGTATTTCCCTGTGCCCTTCTCT  
ATAAAGTCCCTAACCTTCTGCCATTCCAATGTCTGTCTCATCTCACTGTCTTACCAAAA  
CATGATGGCGCTAGCTTGTGCCAGCACCCGCTCAACAGCCTCTACGGCCTCATCTGCTGCT  
ATCTTACACTGGGGCTCGATGTTCTCTCACTCACTGTCTTATGATCACTACCCCTGAAGAC  
TGTGCTGGGCATTTGCTCCAGAGGTGAAAGGCTGAAACCCCTCAGCACATGCTCTCTCAC  
35 ATGTTCACTGCTGCTCTCTCTATGTTCTTTATGGGTGCTGCTCCATGATACACAGAT  
TTGGGACGATTATCACCACTAGTGCACATGGTTCATGGCTGATATATACCTACTGCTCCCG  
CCTGTGCTAAACCCCATGTCTACAGTGTGAAGACCAAGCAAAATTGA (SEQ ID NO: 338)

**AOLFR184 sequences:**

MSLTPTQIAPNSSTSMAPTLLVGMPLSGAPSWWTLPLIAYVLLSALGNGTILWIALQPALHR  
40 PMHFFLLSVSDIGLVTALMPTLLGIALAGHTVPASACLQMVFIHVFSVMESVLLAMSID  
RALAICRPLHYPALTLNVISKISLAISFRCLGLHLPLFLLAYMPYCLPQVLTHSYCLHPDVALL  
ACPEAWGAAYSLFVLSAMGLDPLIFFSYGLIGKVLQGVESREDRWKAGQTCAAHLSAVLLF  
YIPMILLALINHPLEPITQHTHTLLSVVHFLPLPLNPIVSVKMKIEIRKILNRLQPRKVGAQ  
5 (SEQ ID NO: 339)

ATGTCAACATTACCAACTCAGATAGCCCCCAATAGCAGCACTTCAATGGCCCCCACCTTCT  
TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCCTCTGGTGGACATTGGCCCTCATGTTG  
TGCTACCTTCTCTCTGCTACTGGGAAATGGCACCATCTCTGGATCAATTGCCCTGACGCC  
60 GCCCTGCCACGCCCAATGCATCTTCTCTCTTCTGCTTATGTTGTCTGATATTGGATTGGT  
CACTGGCCTGATGCCCACTGCTGGGCATGCGCCTTGGTGTGCTGCACACTGCTCCGCTGC  
TCAGCCTGCCTTCTACAGATGGTTTTATCCATGTCTTTTCTGTCATGGAGTCTCTGTCT  
GCTCGCCATGCTCATTTGATCGGGCACTGGCCATCTGCCGACTCTCACTACCCAGCGCTC  
CTACCAATGGTGTAATTAGCAAAATCAGCCTGGCCATTCTTTTCGATGCTGGGTCTCC  
ATGTGCCCTGCCATTCTGCTGGCCTACATGCCCTACTGCTCCACAGGCTCTAACCCAT  
75 TCTTATTGCTTGCATCCAGATGTGGCTCGTTGGCCTGCCAGAGCTGGGGTGGAGCT  
ACAGCCTATTGTGGTCTTTCAGCCATGGGTGTGAGCCCCCTGCTATTCTTCTCTCTAT

GGCCTGATTGGCAAGGTGTTGCAAGGTGTGGAGTCCAGAGAGGATCGCTGGAAGGCTGGT  
 CAAACCTGTGCTGCCCACTCTCTGCAAGTGTCTCTCTCTATATCCCTATGATCCTCTGGC  
 ACTGATTAAACCATCTCTGAGCTGCAATCACTCAGCATACCCATACTCTCTATCTATGTGC  
 ATTTCTCTCTCTCTCCATTGATAAACCTATCTCTATAGTGTCAAGATGAAGAGATTGACA  
 AAGAAATACTCAACAGGTTCAGCCCCAGGAAGGTGGGTGGTCTCAGTGA (SEQ ID NO:  
 340)

**AOLFR185 sequences:**

MFYPIILNDISTKNNNSIMSCCNILFIKTVIILLVYNQTSQSPWYPIVPSKSLVYNNNTCFDCYHLQR  
 10 VDCVPSRDHINQSMVLASGNSSHPVSFILLGIPGLEFQWLWIAFPFCATYAVAVVGNITLLHVIR  
 IDHTLHEPMYLFLAMLAITDLVLSSTQPKMLAIFWFHAHEIQYHACLIQVFFIHAFSSVESVGL  
 MAMALDCYVATCFPLRHSSILTPSVVIKLGTTVMRLGLLWVSPFCFMSVRMPFCQHQAIQPSYC  
 EHMAVLKLVCAADTISIRGYGLFVAFSVAGFDMIVGMSYVILRAVLQLPSEARLKAFSTRA  
 SHICVILALYIPALFSFLTLYRFGHDVPRVVHILFANLYLLIPMLNPIIYGVRTKQIGDRVQIGCCG  
 15 NIP (SEQ ID NO: 341)

ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTCTGATTT  
 TAAACATATTATTTATTAACACAGTTGAAATTATTTAGTTTATAATCAACACCAATCAACC  
 20 CTGGTATCCAAATAGTCCCATCCAAAAGCCTTGATATAATAATAACACTGTTTGTGATGTT  
 ATCATCTGCAGAGAGTAGATTGCGTTCCAGCAGAGACCATATTAACCACTCCAGTGGTGTG  
 GGCTCAGGGAACAGCTCTTCTCATCTGTGTCCTTCATCTGCTTGAATCCAGGCCCTG  
 GAGAGTTTCCAGTTGTGGATTGCGTTTCCGTTCTGTGCCACGTATGCTGTGGCTGTTGTGG  
 AAATATCACTCTCTCCATGTAATCAGAATTGACCAACCTGCATGAGCCCATGTACCTC  
 25 TTTCTGGCCATGCTGGCCATCACTGACCTGGTCTCTCTCTCCACTCAACCTAAGATGTT  
 GGCCATATCTCGTTTTCATGCTCATGAGATTCACTGACCTGCTGCTCATCCAGTGTCTT  
 TCATCCATGCTCTTTCTCTGTGGAGTCTGGGGTGCTCATGGCTATGGCCCTGGAGCTGCAC  
 GTGGCTACCTGCTCCCACTCCGACACTCTAGCATCTGACCCCATCGGTGCTGATCAAC  
 TGGGGACCATGCTGATGCTGAGAGGGCTGCTGTGGGTGAGGCCCTTCTGCTTCATGGTGTC  
 30 TAGGATGCGCTTGTGCCAACACCAAGCCATTCCCACTGATCACTGTGAGACATGGCTGTG  
 CTGAAGTTGGTGCTGTGCTGATACAAGCATAAGTCTGGGTATGGGCTCTTTGTGGCTCTT  
 CTGTGGCTGGCTTTGATATGATTGTGCTATGGTATGTCACTACGTGATGATTTGAGAGCTGT  
 GCTTCAGTTGCCCTCAGGTGAAGCCCGCTCAAAGCTTTAGCACAGCTGCTCCCATATC  
 35 TGTTGCATCTTGGCTCTTTATATCCAGCCCTTTTCTTCTCTCACTACCGCTTTGGCCAT  
 GATGTGCCCGGAGTTGTACACATCTCTGTTGCTAACTCTATCTACTGATACCTCCCATGCT  
 CAACCCCATCAITTTATGGAGTTAGAACCAACACAGATCGGGGACAGGGTTATCCAAGGATG  
 TTGTGGAACATCCCTGTA (SEQ ID NO: 342)

**AOLFR186 sequences:**

MSNASLVTAFILTLPHAPGLDALLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS  
 40 FIDMWFSTVTVPKMLMTLVSPSGRAISHFSCVAQLYFFHFLGSTCEFLYTVMSYDRLAISLYP  
 RYTSMMSSGSRCALLATGTWLSGSLHSAVQTILTFHLPYCGPNQIQHYFCDAPIILKLACADTSA  
 NVMVIFVDIGIVASGCFVLIVLSYVSIVCSILIRTSIDGRRRAFQTCASHICIVVLCFFVPCVVI  
 PGSMDAMDGVVAIFYVTLTPLNPVYTLRNKEVKKAVLKLRLVAHPQRK (SEQ ID NO:  
 343)

ATGTCCAACGCCAGCCTCGTGACAGCATTCATCCTCACAGGCCCTTCCCATGCCCAAGGGC  
 TGGACGCCCTCTCTTTGGAATCTTCTGGTGGTTTACGTGTCTACTGTGCTGGGGAACCT  
 CCTCATCTGCTGGTGATCAGGGTGGATTCTCACTCCACACCCCATGTACTACTTCTCA  
 50 CCAACCTGCTCTTACATGACATGTGGTTTCCACTGTCAAGGTGCCCAAAATGCTGATGAC  
 CTGGGTGTCCCAAGCGGACAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGTCTATTTTT  
 TCCACTCTCGGGGAGCACCGAGTGTTCCTCTACACAGTCACTGTCTATGATCGCTCACTTG  
 GCCATCAGTTACCGCTCAGGTACACAGCATGATGAGTGGGAGCAGGTGTGCCCTCTGG  
 CACCGGCACTTGGCTCAGTGGCTCTGTCACTGCTGTCCAGACCATATTGACTTCCAT  
 55 TGTGCCCTACTGTGACACCAACAGATCCAGCACTACTTCTGTGACGACGACCCCATCTGA  
 AACTGGCTCTGACAGACACCTCAGCCAAACGTGATGCTACTTTGTGGACATGGGATAGT  
 GGCCTCAGGCTGCTTTGTCTGATAGTGTCTCTATGTGTCACTGCTGTGTCCATCTGCTG



GGATCCGCACTCAGATGGGAGGCGCAGAGCCTTTCAGACCTGTGCCTCCCACTGTATTGT  
GGTCTTTGCTCTTTTGTTCCTGTGTGTCAITTAATCTGAGGCCAGGCTCCATGGATGCCA  
TGGATGGAGTTGTGGCCATTTCACACTGTGCTGACGCCCTTCTCAACCCCTGTTGTGTAC  
ACCCGTGAGAAACAAGGAGGTGAAGAAAGCTGTGTGAAACTTAGAGACAAAGTAGCACAT  
CTCAGAGGAAATAA (SEQ ID NO: 344)

#### AOLFR187 sequences:

MAQVRALHKIMALFSAANSIGAMNNSDTRIAGCFLTGPGLQLHIWLSIPFCIMYIAALENGNLI  
CVILSQAILHEPMYIFLSMLASADVLLSTTMPKALANLWLGYSHISFDGCLTQKFFIHLFIHSA  
VILAMAFDRYVAICSPRYVITLSKVIGKIVTATLSRSFIIMFSPILFLEHLHYCQINIAHTFCEH  
MGIAHLSGSDISINVWYGLAAALLSTGLDIMLITVSYIHILQAVFRLLSQDARSKALSTCGSHICV  
ILLFVYPALFSVFAFYRFGGRSIPCYVHILLASLYVIPPMLNPVIYGVRTKPILEGAKQMFSNLA  
GSK (SEQ ID NO: 345)

ATGGCAGAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTTTTCTGCTAACAGCATAGGTG  
CTATGAACAACTCTGACACTCGCATAGCAGGCTGCTTCCTCACTGGCATCCCTGGGCTGGA  
GCAACTACATATCTGGCTGTCCATCCCTTCTGCAATCATGTACATCGCTGCCCTGGAAGGC  
AATGGCATCCTAAATTTGTGTCATCCTCTCCAGGCCAATCTGCATGAGCCCATGTACATAT  
TCITATCTATGTGCGGCAGTGCTGATGCTTGTCTCTACCAACCCATGCCTAAGGCCCTG  
GCCAATTTGTGGCTAGGTTATAGCCACATTCTTGTATGGCTGACCTCACTAAAAGTCTT  
CATTCATCTCTCTTCACTTCACTGTGCTGCTGCTGGCCATGGCCCTTGACCGCATGTGG  
CCATCTGCTCCCCCTGCGATATGTCACAATCTCACAAGCAAGGTCATGGGAAGATCGT  
CACTGCCACCTGAGCGCGCAGCTTCATCATTTATGTTCCATCCATCTTCTCTGAGCACC  
TGCACTATTGCCAGATCAACATCATTGCACACACATTTTGTGAGCACATGGGCATGGCCCA  
TCTGCTCTGTTCTGATATCTCCATCAATGTCTGGTATGGGTTGCGAGCTGCTCTTCTCTCA  
CAGGCTGGACATCATGTCTATTACTGTTTCTACATCCACATCTCCAAAGCATCTCTCCG  
CTCCTTTCTCAAGATGCGCCCTCAAGGCCCTGAGTACCTGTGGATCCCATATCTGTGTCAT  
CCTACTCTCTATGTCCCTGCCCTTTTTTCTGCTTTGGCTACAGGTTTGGTGGGAGAAGCA  
TCCCATGCTATGTCCATATTTCTCTGGCCAGCCTCTACGTTGTCACTCTCTATGCTCAAT  
CCCGTATTTATGGAGTGAGGACTAAGCAACTGGAAGGGGCTAAGCAGATGTGTTTCA  
AATCTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

#### AOLFR188 sequences:

MEPSLPCVLLVQLPLMNENMQCFVFCSDSLLRMVSRFIHVFPVKMRIIVGGYSKHFFSN  
ELLCVRPWSGKTSIRIHIFDMELLTNLKFITDPFVCRRLRLSPTESEHMKNNNVTEFILL  
GLTQNPQKQLVFTFLIYMTIMGNLLIIVTIMASQSLGSPMYFFLASLSFIDTVYSTAFAPK  
MIVDLLSEKKTISFGQCMCAQFMDHLFAGAEVILLVVMAYDRYMAICKPLHELHIMNRRVCV  
MLLAWIGGFTHSLVQFLFIYQLPFCGPNVIDNFLCDLYPLLKLACTNTYVTLGSMIANGCA  
AVTFTTILLSYGVLVHSLKTSLEGRKRAFYTCAASHVTVVILFVFPICFLYARPNSFTPIDKSMV  
VLTFTPMLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLYHS (SEQ ID NO: 347)

ATGTTCCCTCCCTGTGTCCATGTGTTCTCTTGTTCAACTCCCACTTATGAATGAGAACAT  
CGAGTGTGTTGTTTCTGTTCTGTGATAGTTTGTGAGAATGATGGTTTCCCGCTTCACTCC  
ATGTCCATTTGTAAAAATGAAAAGGATAAATTTGGGGAGGATATCTTAAACACTCTTCTTTC  
TAATGAGCTGCTGTGTGAGGCCCTGGTCAGGGAAAAAGGTTTATTTTGTGACAT  
TTTGACATGGAGCTTCTGACAAAAATCTCAAAATTTTCACTGACCCCTTTTGTGTAAGGC  
TCCGACACCTGAGTCCAAACACCTTCAGAAGAACACATGAAAAATAGAACAATGTGACTG  
AATTATCTCTTAAGGGCTCACACAGAACCTGAGGGGCAAAAGGTTTATTTTGTGACAT  
CTTACTAATCTACATGGTGACGATAAATGGGCAACCTGCTTATCATAGTGACCATCATGCGC  
AGCCAGTCCCTGGGTTTCCCCATGTACTTTTTCTGGCTCTTATCATGATCATAGATACCGT  
CTATTCTACTGCATTTGCTCCCAAAATGATTGTTGACTTGCTCTCTGAGAAAAAGACCATTT  
CCTTTAGGGTTGATGCTTCACTTTTATGGATCATTTATTTGCTGGTGTGTAAGTCACT  
CTTCTGGTGAATGGCCTATGATGATACATGGCCATCTGTAAGCCCTTCTCATGAATTGA  
TCACCATGAATCGTGGAGTCTGTGTTCTTATGCTGTTGGCGGCTGGATGGAGGCTTCTCT  
TCACATCTGGTTCAATTTCTCTTTATTTATCAGCTCCCTTCTGTGGACCAATGTGCTATG  
ACAACCTCTGTGTGATTGTATCCCTTATTTGAAACTTGCTTGACCAATACCTATGTCACT

GGGCTTTCTATGATAGCTAATGGAGGAGCGATTGTGCTGTCACCTTCTTCACTATCCTGC  
TTTCTCATGGGGTCATATTACACTCTCTTAAGACTCAGAGTTTGGGAAGGGAACGAAAGCG  
TTTCTACACCTGTGCATCCCACGTCACGTGGTGCACTTTTATCTTTGTGCCCTGTATCTTCTT  
GTATGCCAAGGCCAATTCTACTTTTCCCATTTGATAAAATCCATGACTGTAGTTCTAATCTTTA  
5 TAAGTCCCATGCTGAACCCCACTAACTCTATACCGTGAAGAAATGCAGAAATGAAAAGTGCCAT  
GAGGAAACTTTGGAGTAAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA  
(SEQ ID NO: 348)

**AOLFR189 sequences:**

10 MQQNNVSPFILLGLTQDPLRQKIVFVIFLIFYMGTVVGNMLIIVTIKSSRTLGSMPYFFLYLSE  
ADSCFSTAPRLIVDALSEKKIITYNECMTQVFAHLHFGCMEIFVLILMAVDRYVAICKPLRYP  
TIMSQQVCHILIVLAWIGSLIHSTAQILALRPFPCGPLYIDHYCCDLQPLLKLACMDTYMINLLL  
VNSNGAICSSSFILIIYSYIVILHSLRNHSAKGKKKALSACTSHIIVVILFFGPCIFYTRPPTTFPMD  
KMWAVFYITGTPFLNPLIYTSECRSEKCHEK (SEQ ID NO: 349)

15 ATGCAGCAAAATAACAGTGTGCCTGAATTCTACTGTTAGGATTAACACAGGATCCCTTGA  
GGCAGAAAATAGTGTTTGTAATCTTCTTAATTTCTATATGGGAACCTGTGGTGGGGAATAT  
GCTCAITATTGTGACCATCAAGTCCAGCCGGACACTAGGAAGCCCATGTACTTCTTCTA  
20 TTTTATTTGTCCTTTGCAGATTCTTGCTTTTCAACTTCCACAGCCCTAGATTAAITGTGGA  
TGCTCTCTCTGAAAAGAAAATTATAACCTACAATGAGTGATGACACAAGTCTTTGCACATA  
CATTATTTGGCTGCATGGAGATCTTTGTCTTCATTCTCATGGCTGTTGATCGCTATGTGGC  
CATCTGTGAAGCCCTTGCGTTACCCAACCATCATGAGCCAGCAGGTCTGCATCATCTCTGATT  
30 GTTCTTGCCCTGGATAGGGTCTTTAATACACTCTACAGCTCAGATTATCCTGGCCTTAAGATT  
GCCCTTCTGTGGACCCATTTGATTGATCATTATTGCTGTGATTGACAGCCCTGTGTGAAAC  
25 TTGCGTGCATGGACACTATACATGATCAACCTGCTGTTGGTGTCTAACAGTGGGGCAATTGT  
CTCAAGTAGTTTCATGATTTTGATAATTTTCATATATTGTCATCTTGCATTCACGAGAACC  
ACAGTGCCAAGGGGAAGAAAAAGGCTCTCTCCGCTTGACAGTCTCACATAATTGTAGTACT  
CTTATCTTTGGCCCATGTATATTCTATATATACACGCCCCCGACCACTTTCCCATGTGGACA  
AGATGTTGGCAGTATTTTATACTATTGGAACACCCCTTCTCAATCCACTCATCTACACATCT  
30 GAGGAATGCAGAAGTGA AAAATGCCATGAGAAAG (SEQ ID NO: 350)

**AOLFR190 sequences:**

MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVYCLTVVGSSTLIVLCNDSRLHTPMYFVIGN  
LSFLDLWYSSVHTPKILVTCISEDKSISFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL  
35 YAQTMPRLCICLVLYSYTGGFVNAILTSNFTLDFCGDNVIDDFCDVPLVKLACSVRESYQ  
AVLHFLASNVISPTVLILASYSIIITTLRIHSTQGRIKVFSTCSSHLSVYTLYYGSILYNSRSPSS  
YSLKRDKMVSTFYITMLFPMLNPMIYSLRSKDMKDALKKFFKSA (SEQ ID NO: 351)

ATGCAGAGGAGCAATCACACAGTGACTGAGTTCATCTGCTGGGCTTACCACAGATCCAG  
40 GAGTGCAACTGGGCCCTCTTTGTGGTGTCTCTGGGTGTGACTGTCTGACTGTGGTAGGAAG  
TAGCACCGCTCATGCTGTGATCTGTGAATGACTCCCGCTACACACACCCATGTATTTTGTCA  
TTGGAAATCTGTCAATTTCTGGATCTCTGGTATTCTTCTGTCCACACCCCAAGATCTCTAGTG  
ACCTGCATCTCTGAAGACAAAAGCATCTCCCTTGTCTGGCTGCTGTGTCAGTTCTTCTCTGC  
CAGGCTGGCCTATAGTGAGTGCTACTCTGGCTGCCATGGCTTATGACCACTACGTGGCC  
45 ATCTCCAAGCCCTTGCTTTATGCTCAGACCATGCCAAGGAGATTGTCATCTGTTTGGTTT  
ATATTCTATACCTGGGGGTTTGTCAATGCAATAATATTAACAGCAACACATTACATTG  
GATTTTTGTGGTGACAAATGTGATTGATGACTTTTCTGTGATGTTCCACCCCTCTGGAAGCT  
GGCATGCACTGTGAGAGAGAGCTACCAAGCTGTGCTGCACCTCTCTTGCCCTCCAATGTG  
50 ATCTCCCTCATGCTGCTCATCTTGCCTCTTACCTCTCCATCATACACCACTGCTGAGGAT  
CCACTCTACCCAGGCCGCATCAAAAGTCTTCTCCACATGCTCTCCCACTGATCTCCGTTA  
CCTTATACATATGGCTCCATTCTTACAACACTCTCCCGCCAAAGTCCAGCTACTCCCTCAAG  
AGGGACAAAATGGTTTCTACCTTTTATACTATGCTGTTCCCATGTGATGTAATCCCATGATCTA  
CAGCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATTCTTCAAGTCAGCATAA  
(SEQ ID NO: 352)

55

**AOLFR191 sequences:**

MTGGGNTBITYFILLGFSDFPRIIKVLFTIFLVYITSLAWNLSLVLIRMDSHLHTPMYFFLSNLS  
FIDVCYISSTVPKMLSNLLQEQQTTTFVGCIIQYFIFSTMGLSECLMTAMAYDRYAAICNPLLYS  
SIMSPITLCVWMVLGAYMTGLTASLQIGALLQLHFCGSGNVIRHFFCDMPQLLILSCTDITFFVQV  
MTAILTMFFGIASALVIMISYGYIGSIMKITSAKGSPPKAFNTCASHLTAVSLFYTSGIFVYLRSSS  
GGSSSDFRFAVVFYTVVIMPLNPLIYSLRNKEIKDALKRLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTCATCCTGCTGGGATTCTCAGATT  
TTCCCAAGGATCATAAAAGTGCTCTTCACTATATTCCTGGTGATCTACATTACATCTCTGGCC  
TGGAACTCTCCCTCATTTGTTTAAATAAGGATGGATTCCCACCTCCATACACCCATGTATT  
CTTCCTCAGTAACCTGTCTCTCATAGATGTCTGTATATCAGCTCCACAGTCCCCAAGATGC  
TCTCCAACCTCTTACAGGAACAGCAAACCTATCACTTTTGTGGTGTGATTATTCAGTACTTT  
ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCATGACAGCCATGGCTTATGATCGTT  
ATGCTGCCATTGTAAACCCCTGTCTATTCACTCCATCATGTCAACCCACCTCTGTGTTTGGT  
15 ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTTATCCAAATTTGGTGCTTTGCT  
TCAACTCCACTTCTGTGGGTCTAATGTCATCAGACATTTCTTCTGTGACATGCCCAACTGT  
TAATCTGTGCTGTATGACACTTCTTTGTACAGGTCATGACTGCTATATTAAACCATGTTCT  
TTTGGGATAGCAAGTGCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA  
TGAAGATCACTTCAGCTAAAGGCCAGTCCAAAGGCATTCAACACCTGTGCTTCTCATCAAC  
20 AGCTGTTTCCCTCTTCTATACATCAGGAATCTTTGTCTATTGAGGTCAGCTCTGGAGGTT  
CTTCAAGCTTTGACAGATTGTCATCTGTTTCTACACTGTGGTCAATCCCATGTTAAATCCC  
TGAGTTACAGTTTGAGGAACAAAGAAATTAAGATAGCCTTAAAGAGGTTGCAAAAGAGA  
AAGTGCTGCTGA (SEQ ID NO: 354)

**AOLFR192 sequences:**

MENNTVEVTEFILVGLTDDPELQIPLFIVFLFIYILITLVGNLGMIELLLDSCSLHTPMYFFLSNLSLV  
DFGYSSAVTPKVMVGLTGDKFILYNACATQFFFFVAFITAESFLLASMAVDRYAALCKPLHY  
TTTMTTNVCACLAIGSYICGLFNASHITGNFRLSFCRSNVVEHFFCDAPPLLTSCSDNYISEM  
VIFVVFVGFNDLFSILVILISYLFITITMKMRSPGGRKQAFSTCASHLTAVSIFYGTGIFMYLRPNSS  
30 HFMGTDKMASVFYAIVIMPLNPLVYSLRNKEVKSFAFKKTVGKAKASIGFIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTCATCCTTGTTGGGGTTAACTGATGACCCAGAA  
CTGCAGATCCCACCTCTTCATAGTCTTCCTTTTCATCTACCTCATCACTCTGGTTGGGAACCT  
GGGGATGATTGAATTGATTCTACTGGACTCTGTCTCCACACCCCATGTACTTCTCTCTCA  
35 GTAACCTCTCCCTGGTGACTTTGGTTATCTCTCAGCTGTCACTCCCAAGGTGATGGTGGG  
GTTTCTCACAGGAGACAAAATTCATATTATATAATGCTTGTGCCACACAATTCTTCTCTTTG  
TAGCCTTATCATCTGCAGAAAGTTTCTCTCTGGCATCAATGGCCTATGACCCGATATGCAGC  
ATTGTGTAAACCCCTGCATTACACCACCAACCATGACACAAATGTATGTGCTTGGCTGGCC  
ATAGGCTCTCATCATCTGTGGTTTCTCGAATGCATCCAATCATACTGGGAACACTTTCAGGC  
40 TCTCCTTCTGTAGATCCAATGTAGITGAACACTTTTCTGTGATGCTCCTCCTCTCTTGA  
CTCTCATGTTTCAGAACACTACATCAGTGAGATGGTATTTTCTTGTGGTGGGATTAAGT  
ACCTCTTTCTATCTCGGTAATCTGTATCTCCTACTTATTTATTTATTCACCATCATGAAG  
ATGCGCTCACCTGAAGGACGCCAGAAGGCCITTTCTACTTGTGCTTCCACCTTACTGCA  
TTTCCATCTTTTATGGGACAGGAATCTTATGTACTTACGACCTAACTCCAGCCATTTTCATG  
45 GGCACAGCAAAATGGCATCTGTGTCTTCTAGCCATAGTCAATCCCATGTTGAATCCCATGG  
TCTACAGCCTGAGGAACAAAGAGGTTAAGATGTCCTTTAAAGAGCTGTAGGGAAGGCCAA  
AGGCCTCTATAGATTTCATATTTAA (SEQ ID NO: 356)

**AOLFR193 sequences:**

MENKTEVTQFILLGLTNDSELQVPLFTTFPIYIITLVGNLGIHVLIFWDSCLHNPMYFFLSNLSLV  
DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYIFVAFATVENYLLASMAVDRYAALCKPLHY  
TTTMTTTCARLALIGSYLCLGFLNASHITGDTFSLFCCKSNEVHFFCDIPAVMLVSCSDRIHSEL  
VLIVVVSFNIFIALLVILISYTFITILKMHSAVYQKPLSTCASHIAGVIFGTGIFMYLQPSHSH  
SMDTDKMAPVFVTMVIPLNPLVYSLRNKEVKSFAFKKVVEKAKLSVGWSV (SEQ ID NO:  
357)

ATGGAAAATAAGACAGAAGTAACACAATTCATTCTTCTAGGACTAACCAATGACTCAGAA  
CTGCAGGTTCCCTCTTTTATAACGTTCCCTTTCATCTATATTATCACTCTGGTTGGAAACCT  
GGGAATTATTGTATTGATATTCTGGGATTCTGTCTCCACAATCCCATGTACTTTTCTCA  
GTAACATTGTCTCTAGTGGACTTTTGCTACTCTTCAGCTGTCACTCCCATCGTCATGGCTGGA  
5 TTGCTTATAGAAGACAAGGTCATCTCTTACAATGCATGTGCTGCTCAAAATGTATATCTTTGT  
AGCTTTTGCCACTGTGGAAAAATTACCTCTTGGCCTCAATGGCCATGACCGCATGCGAGCA  
GTGTGCAAAACCCCTACATTTACACCACAACCATGACAACAACCTGTGTGCTGCTGTGGCCA  
TAGGCTCTCACTCTGTGGTTTCTGTAATGCCCTCCATCCACACTGGGGACACATTTAGTCTC  
TCTTCTGTAAGTCCAATGAAGTCCATCACTTTTCTGTGATATTCAGCAGTCTATGGTCTGA  
10 CTCTTGCTCTGATAGACATATTAGCGAGCTTGTCTTATTTATGTGTGAGCTCTCAATATCT  
TTATAGCTCTCTGGTTTATCTTGATATCTACACATTCATTTTATCAACCTCAATAAGATG  
CACTCAGCTCTGATATACAGGAAGCCTTTGTCCACCTGTGCTCTCAATTTTCATTGCGAGTCGG  
CATCTTCTATGGGACTATTATCTTCTATGTACTTACAACCCAGCTCCAGTCACTCCATGGACA  
CAGACAAAATGGCACTGTGTCTATACAATGGTCATCCCCATGCTGAACCCCTCTGGTCTA  
15 TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT  
GTCTGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

#### AOLFR194 sequences:

MERQNSQCVFEILLGFSNYPELQQLFVAFVLYIYVLTIGNAHIVSLVDQSLHVPMLYFLNLL  
20 SVVDLSFSAVIMPEMLVVLSTEKTTSFGGCFQAMYFILLFGGAECFLLGAMAYDRFAAICHPL  
NYQMIMNKGVFMKLHFSWALGFMLGTVQTSWVSSFPFCGLNEINHISCTPAVLELACADTFL  
FEIYAFGTGFLILVPLLLSIRVLFALIKMPSITGRQKAFSTCAAHLSVTLYFTGASMTYLLQ  
PKSGYSPETKKVMSLSYLLTPLLNLIIYSLRNSSEMKRALMKLWRRRVVLHIT (SEQ ID NO:  
359)

ATGGAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCTCTTGGGCTTTTCTAACTATC  
CTGAGCTCCAGGGGCACTCTTTGTGGCTTCTCGGTATTTATCTGTGTGACCCCTGATAGG  
AAATGCCAATTATTAGTCATCGTCTCCCTAGACCAGACGCTCCACGTTCCCATGTACCTGT  
30 TTTCTCTGAACCTATTCTGTGGTGGACCTGAGTTTCAAGTGCAGTATTATGCTCGAAATGCT  
GGTGGCTCTCTCTACTGAAAAAACTACAATTCTTTTGGGGGCTGTTTGGCAGAGATGTAT  
TTCATCTCTCTTTTGGTGGGGCTGAATGTTTCTTCTGGGAGCAATGGCTTATGACCGAAT  
CTGTGCAATTTGCCATCCTCTCAACTACCAATGATTATGAATAAAGGAGATTTTATGAAA  
TTAATTATATTTTCTGAGGCTTAGGTTTATGTAGGTAAGTGTCAAACATCATGGGTATC  
35 TAGTTTCCCTTTTGTGGCCTTAATGAAATTAACCATATATCTTGTGAAACCCAGCAGTGT  
TAGAATCTGCATGTCGACACACGTTTGTGTTGAAATCTATGCATTACAGGCACTTTTGTG  
ATTATTTGGTTCCTTTCTGTTGATACCTTGTCTTACATTGAGTCTGTTTGCCATCCTG  
AAGATGCCATCAACCACTGGGAGACAAAAGGCCTTTCCACCTGTGCCGCTCACTCAGT  
CTGTGACCTTATCTATGGCAGCAGCAGTATGACTTATTTACAACCCAAATCTGGCTACTC  
40 ACCGGAAACCAAGAAAGTATGTCATTGTCTTCACTCTGACCACTGCTGAATCTG  
CTTATCTACAGTTTGGCAATAGTGAGATGAAGAGGGCTTGTATGAAATATGCGCAAGG  
CGAGTGGTTTTACACACAATCTGA (SEQ ID NO: 360)

#### AOLFR195 sequences:

MIVQLICTVCLAVNTHVRSSFDLKLADDMEINQTLVSEFLLGLSGYPKIEIVYFALILVMY  
45 LVILIGNGVLIASIFDHFHTPMYFFLGNLSFLDICYTSSSVPSLTVLSLKKRNISFGCAVQMFF  
GFAMGSTECLLLGMMAFDRYVAICNPLRYPILSKVAVYVLMASVSWLGGINSVAQVLLAMRL  
PFCGNINHFACELAVLKLACADISLNIITMVISNMAFLVPLMVIFSYMFILYTLQMSNATG  
RRKAFTSCSAHLTVVIFVGTIFFMYAKPKSQDLIGEELQLADKLISLFYGVYVTPMLNPILYSRL  
NKDVKAALKVYLLNKKPIH (SEQ ID NO: 361)

ATGATTGTTCAGTTAATTTGTACTGTTTGTCTTGGCAGTAAATACATTTCACTGTAGATC  
TTCCTTTTGATTTCTGAAAGCAGATGACATGGGTGAGATTAAACGACACTGTGTGTCAGAA  
TTCTCTCTCTGGGTCTTCTGGATACCCAAAGATTGAGATTGTTTACTTCTGCTCTCAITCT  
AGTTATGTACCTAGTGTATCTAAITGGCAATGGTGTCTAACTATGACCGCACTCTTGAT  
55 TCAATTTTACACACCAATGTACTTCTCTGGGCAACCTCTTCTTCTGGATATCTGCTAT  
ACATCTCTCTGTTCCCTCAACATTTGGTGAGCTTAATCTCAAAGAAAAGAAACATTTCTCT

5 TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGCAATGGGGTCAACAGAAATGCTGCT  
TCTTGGCATGATGGCATTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC  
ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTCTGTGTCTGGCTGTCCGGTGGAAATA  
TTCAGCTGTGCAAAACATTACTTGCCATGAGACTGCCTTCTGTGGGAATAATATTATCAA  
10 ATATTTCGCATGTGAAATATTAGCTGTCTCAAGCTGGCCTGTCTGATATATCCCTCAATA  
TATTACACCATGGTGATATCAAAATAGGCCCTTCTGGTCTTCCACTGATGGTCATTTTTTC  
TCCTATATGTTCATCCCTCAACCATCTTGCAAATGAATTCAGCCACAGGAAGCCGAAG  
CATTITTCACGCTGCTCAGCTCACCTGACTGTGGTGATCATATTTACGGTACCATCTCTTT  
ATGTATGGGAAACCGAAGTCTCAAGACCTGATTGGGGAGAAAAATTCGAAGCATTAGAC  
15 AAGCTCATTTCTCTGTTTATGGGGTAGTGACACCATGCTGAATCCTATCTCTATAGCTT  
GAGAAATAAGGATGTAAGAGCTGCTGTAAATATTTGCTGAACAAAAACCAATCTACTA  
A (SEQ ID NO: 362)

# **AOLFR196 sequences:**

15 MLESNYTMPTEFLFVGFDTYDPLRVTLFLVFLVYLTLMVGNILLVLNINSSLIQPMYYFLSNL  
SFLDISCSATITPKMLANFLASRKSISPYGCALQMEFFAFADAECLILAAAMYDRYAAICNPIL  
YTLTMSRRVCVFIVLAYFSGSTTSLVHVLCFLRFLSCGSNIVNHFFCDIPPLLALSCTDQINQL  
LLFALCSQITSTFVVFISFYCILITVLSIKSSGGRSKTSTCASHLIATVLFYGALLFMYLQPTTS  
YSLDTRKVVAVFYTVVFPFMPNPIYSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ  
20 ID NO: 363)

ATGTGGAGAGTAATTACACCATGCCAACTGAGTTCCTATTGTTGGATTACAGATTATC  
TACCTCTCAGAGTCACACTGTTCTTGGTATTCCTTCTGGTATATACATTAACATTAAGTGGTCGGA  
25 AATATACCTTTAATAATCTAGTTAATATTAATCAAGCCCTCAAAATCCCATGTATTATT  
TCTTAGCAACTTATCTTTCTTAGACATCAGCTGTCTACAGCAATCACTCTAAAATGCTGG  
CAAACTCTTGGCATCCAGGAAAAGCACTCTCCTTATGGGTGTGCATCAAAATGGTTTT  
CTCGCTTCTTTTGTCTGATGCTGAGTGCCTTATCCIGGCAGCAATGCGCTATGACCGCTATG  
CAGCCATCTGCAACCCACTGCTCTATACTACACTGATGTCTAGGAGAGTCTGTGTCTGCTT  
30 CATGTTGTGGCATATTTCAAGTGAAGTACAACACTGCTGCTCATGTTGCTTCACTTCT  
AGGCTGTCAATTTTGTGGCTCAATATCGTCAATCATTTTCTGTGATATCCCACTCTCTCT  
GGCTTTATCATGTACAGACACTCAGATCAACAGCTCTGCTCTTGTCTTTGTGACGCTTCA  
TCCAGACCGACGACTTTTGTGGTAATTTATTTCTTACTTCTGCACTCCTATCATGCTGTGTTG  
AGCATCAAGTCTCAGGTGGCAGAAAGCAAAACATTCTCCACTTGTGCTTCCCACTCATAG  
35 CAGTCACTTATTTCTATGGAGCGCTCTGTTTATGTACTTACAGCCCACTCATGCTATTCC  
CTAGACACTGATAAGGTGGTGGCAGTGTTTTATCATGTTGATTTTCCATGTTTAAATCCAA  
TAATTTATAGTTTTCAGAAAACAGGATGTGAAAAATGCTCTCAAAAAGCTATAGAAAGAA  
TTGCTATTTCAATGTAATGGTATTTAAATCGTTTAAAGAAATAGTCAATATCTAA (SEQ ID NO:  
364)

# **AOLFR197 sequences:**

40 MCYLSQLCLSLGHEHTLHMGMVRHTNESNLGIFLLGFSYPQLQKVLVFLVILYLLTILGNITI  
ILVSRLEPKLHMPMYFLLSHLSFLYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLYNSHALGS  
TECVLLALMSCDRYVAVCRPLHYTVLMHIIHLCMALASMAWLSGIATTLVQSTLTLLQFPFGH  
ROVDHFICEVPVLKLACVGTITNEAELEFVASILFLVFPVSSGYIAHVAFLRIKSTARQKAF  
45 GTCRSHLTVVTFYGTIIFMYLQPAKRSRSDQGFVSLFYTVVTRMLNPLYITLRIKEVKGALK  
VLAKALGVNLI (SEQ ID NO: 365)

ATGTGTTATCTTTCTCAGCTATGCCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG  
TGAGACATACCAATGAGAGCAACCTAGCAGGTTCATCTCTTTTAGGGTTTCTGATTATCC  
50 TCAGTACAGAAGGTCTATTTGTGCTCATATGATCTGTTATTACTAACTATTTTGGGGA  
ATACACCAATCATTTCTGGTTTCTGCTTGGAACCAAGCTTCATATGCCGATGATTTCTTCTC  
CTTCTCATCTCTCTCTCTGTAACGCTGCTTCCAGCAGTGTATATCCCGAGCTCTGGT  
AAACCTGTGGGAAACCAATGAAAACATCGCCTATGGTGGCTGTTTGGTTCACCTTTACAAC  
TCCCATGCCCTGGGATGCACTGAGTGCCTCTTGGCTCTGATGCTCTGTGACCCGCTATGT  
55 GGCTGTCTGCCGCTCTCTCATTTACACTGTCTTAATGCATATCCATCTCTGATGGCCTTGG  
CATCTATGGCATGGCTCAGTGAATAGCCACCACCTGGTACAGTCCACCCTCACCCTGCA

- GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTTCATCTGCGAGGTCCTGTGCTCATC  
AAGCTGGCTTGTGTGGGCACCAAGTTTAAACGAGGCTGAGCTTTTGTGGCTAGTATCTCTT  
TCCTTATAGTGGCTGTCTCATTCATCTGGTCTCTGCTGACATTTGCCACCGAGGTGTG  
AGGATTAAGTCAGCTACCAGGAGACAGAAAGCATTCGGGACCTGCTTCTCCACCTGACA  
GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCAGCCAAGAGTAGAT  
CCAGGGACAGGGCAAGTTTGTCTCTCTCTACACATGTGGTAAACCCGATGCTTAACCC  
TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGGCAATTAAGAAAGTTCTAGCAAA  
GGCTCTGGGAGTAAATATTTTATGA (SEQ ID NO: 366)
- 10 **AOLFR198 sequences:**  
MENCTEVTKILLGLTSVPELQIPILFILFTFIYLLTCLGNLGMMLLLMDLSLHPTMYFFLSNLSL  
VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFFVALATVENYLLASMAVDYRAAVCKP  
LHYTTTMTASVGACLAGLSYVCGFLNASFHIGGIFSLFSCKSNLVHHFCDVPVAVMALSCSDKH  
TSEVLVFMSSFNIFVLLVIFISYLFIFITILKMSAKGHQKALSTCASHFTAVSVFYGTVIFIYLG  
PSSSHSMDTDKMASVFYAMIPLNPNVYSLRNVQNAFFKVLRRQKFL (SEQ ID NO: 367)
- 20 ATGGAGAATTGTACGGGAAGTGACAAAGTTCATCTTCTAGGACTAACCAAGTGTCCAGAAC  
TACAGATCCCCCTCTTTATCTGTGTACCTTCATCTACCTCTCACTCTGTGTGGGAACCTG  
GGGATGATGTGTGCTGATCCTGATGGACTCTGTCTCCACACCCCATGTACTTTTCTCTCAG  
TAACCTGTYCTCTGGTGGACTTTGGATACTCTCAGCTGTCACTCCCAAGGTCAAGCTGGG  
TTCTCTAGAGGACAGCAAGGTCATCTCTCAATGCGATGTGCTGTTCAGATGTCTCTTTGT  
AGCCTTGGCCACGGTGGAAATTAATCTGTGTGGCTCAATGGCCTATGACCGCTATGACGCA  
GTGTGCAAAACCCCTACACTACACCACCACTGACGGCCAGTGTAGGTGCTGTCTGTGGCC  
TAGGCTCATATGTCTGTGGCTTCTAAATGCTCATTTCCACATTTGGGGGACATATTCAGTCTC  
25 TCTTCTGTAAATCCAATCTGGTACATCACTTTTCTGTGATGTTCCAGCAGTCATGGCTCT  
GTCTGTCTCTGATAAACACACTAGTAGGAGTATCTGTGTTTATGTCAAGCTTTAATATCT  
TTTGTGCTCTTCTAGTTATCTTTATCTCCTACTGTTCATATTCATACCATCTGAAGATGC  
ATTCAGCTAAGGGACACAAAAAGCATTTGCCACCTGTGCTCTCACTTCACTGCAGTCTC  
CGTCTTCTATGGGACAGTAACTTTCATCTACTTGACGCCACAGCTCCAGCCACTCCATGGAC  
30 ACAGCAAAATGGCATCTGTGTCTATGCTATGATCATGCCATCCCCATGCAACCCGTGTGGTCT  
ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAGAAAGTGTGAGAAGGCAAAAT  
TTCTATAA (SEQ ID NO: 368)
- 35 **AOLFR199 sequences:**  
MDTGNKLTQDFLLLGFPQSQTLLQLSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS  
NLSFLEIWIYTAAPVKALAILLGRSQTISFTSCLLQMYFVFLGCTEYFLLAAMAYDRCLAICY  
LHYGAIMSSLLSAQLALGWSVCGFVAIVPTALISGLSFCGPRAINHHFCDIAPWIALACTNTQA  
VELVAFVIAVVVLLSCLITFVSYYIISTILRIPASGRSKAFSTCSSHLTVVLIWYGSTVFLHVR  
TSKDALDLIKAVHVLNTVTVPLNPFYTLRNKEVRETLKKWKGE (SEQ ID NO: 369)
- 40 ATGGACACAGGCAACAAAACCTCTGCCCCAGGACTTTCTCTTACTGGGCTTTCTGGTCTCTC  
AAACTCTTACGCTCTCTCTCTTTATGCTTTTCTGGTGTATGATCTCTACAGTATAGTGTG  
AATGTGGCTATCTTGATGTGTGGTGGACACCTCCCATCAGTTGCATACCCCATGTACTCTT  
TCTGAGCAACCTCTCTCTCTGGAGATTGGTATACCACAGCAGCAGTGGCCAAAGCACTG  
45 GCGATCTACTGGGGAGAAGTCAGACCATATCATTTACAAGCTGTCTTTTGACAGTGTACT  
TTGTTTCTCATTAAGCTGCACAGAGTACTTCTCTGGCAGGCATGGCTTATGACCGCTGT  
TCTGCCATCTGCTATCTTTTACACTACGGAGCCATCATGAGTAGCCTGTCTCAGCGCTG  
TGGCCCTGGGCTCTGGGTGTGTGGTTCGTGGCCATTGACAGTGCCACAGCCCTCATCAG  
TGGCTCTCTCTCTGTGGCCCGCGTGCATCAACCACTTCTCTGTGACATGCAACCTGTGA  
50 TTGCTCTGGCTCTGCACCAACACACAGGCAGTAGAGCTTGTGGCCTTTGTGATGTGCTGTG  
GGTATCTCTGAGTATGCTCTCATCCTTTGTCTCTATGTGTACATCATCAGACCATCTC  
TCAAGATCCCTCTGCGAGTGGCCGGAGCAAAAGCCTTCTCCAGCTGCTCTGTGATCTCAT  
CGTGGTCTCATTGTGATGGGTCCACAGTTTTCTCTCAGCTCCGACCTCTATCAAAAGAT  
GCCTTGGATCTGATCAAAGCTGTCCACGTCTGAAACACTGTGGTGACTCAGCTTTTAAACC  
55 CCTTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG  
GAAAAATAA (SEQ ID NO: 370)

#### AOLFR200 sequences:

5 MTRKNYTSLETFVLLGLADTLELQIILFFLVYITLTVLGNLGMILLIRIDSOLHPTMYFFLANL  
SFVDVCSNTTTPKMLADLLSEKKTISFAGCFLQMYFFISLATTECILFGLMAYDRYAAICRPLL  
YSLIMSRVTYVKMAAGAAFAAGLLNFMVNTSHVSSLPDCDSNVIIHFFCDSPPLFKLSCSDTILKE  
SISLLAGVNVIGTLLVLSSYSYVLFISFMSHSGEGRHAFSTCASHLTAIILFYATCIYTYLRPSS  
SYSLNQDKVVASVFYTVVIPMLNPLIYSLRSKEVKKALANVISRKRKTSSEL (SEQ ID NO: 371)

10 ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCTATTGGGATTAGCAGACACGG  
TGGAGCTACAGATTATCCTCTTTTGTGTTTCTTGTTGATTTATACACTACAGTACTGGGA  
AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCAGCTTCACACACCAAGCTATTCTT  
CCTGGCTAACCTGTCCCTTTGTGGACGTTGTAACTCAACTACCATCACCCCAAGATGCTG  
GCAGATTTATTATCAGAGAAGAAAACCATCTCTTTGCTGGCTGCTTCTACAGATGTACT  
15 TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCTTTGGGTTAATGGCCTATGACAGGTA  
TGGCGGCATATGTGCGCCGCTGCTTACTCCTTGATCATGTCCAGGACCGCTACCTAAAA  
ATGGCAGCCGGGGCTTTTGCTGCAGGGTTGCTGAACCTCATGGTCAACACCAAGCCATGTCA  
GCAGCTTGTCATCTTGACTCCAATGTCAATCCTCACTTCTCTGTGACAGTCCGCCACTT  
TCAAGCTCTCTTGTCTGACACAATCCTGAAAGAAAGCATAAAGTTCTATTGGCTGGTG  
TGAATATTGTGGGGACTCTGCTTGTCATCCTCTCCTCACTCCTACGTTCTCTTCTCAATT  
20 TTTCTATGCATTGGGGGAGGGGAGGCACAGAGCTTCTCCACGTGTGCCCTCACTCA  
CAGCATTAATTCTGTCTATGCCACCTGCATCTATACTACCTGAGACCTAGTTCAGCTAC  
TCCCTGAATCAGGAAGAAGTGGCTTCTGTGTTCTACACAGTGGGATTCCTCATGTTAACT  
CTCTGATCTACAGCCTCAGGAGTAAGGAAGTAAAGAAAGGCTTTAGCGAATGTAATGACA  
GGAAAGGACCTCTTCTTTCTGTGA (SEQ ID NO: 372)

25

#### AOLFR201 sequences:

30 MEWENHTILVEFFLKLGLSGHPRLLELFFVLIFIMYVILLNGTLLILSILDPHLHTPMYFFLGNL  
SFLDICYTTTSPSTLVSLSERKTISLSCAVQMFLGLAMGTTECVLGLGMMAFDRYVAICNPLR  
YPIIMSKDAVYVMAAGSWIIGAVNSAVQSVFVQLPFCRNNIINHFTCEILAVMKLACADISDN  
EFIMLVATLFLILPLLLIIVSYTLIIVSIFKISSSEGRSKASSTCAHLTVVIIFYGTILFMYMKPKS  
KETLNSDDLLDATDKIIMFYGVMTMPMNPLIYSLRNKDVKEAVKHLNRRFFSK (SEQ ID NO:  
373)

35 ATGGAATGGGAAAAACACACCATTTCTGGTGGAATTTTTTCTGAAGGGACTTTCTGGTCACC  
CAAGACTGTAGTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTCTGGGG  
AATGGTACTCTCATTTTAAATCAGCATCTGGACCTCACCTTCACACCCCTATGTACTTCT  
TCTGGGGAACTCTCCTCTCTGGACATCTGTACACCAACCACTCTATTCCCTCCACGCTAG  
TGAGCTTCTCTTCAGAAAGAAAGACCAATTCCTCTTCTGGCTGTGACGTGCAGATGTCTCT  
40 CGGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCAT  
GTGGCATCTGTCAACCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA  
TGGCAGCTGGGTCTCGGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTGTGGT  
ACAATTGCCTTTCTCGAGGAATAACATCATCAATTCACCTGTGAAATCTTGGCTGTG  
ATGAACTGGCCTGTGCTGACATCTCAGACAATGAGTTTCATCATGCTTGTGGCCACAACAT  
TGTTTCATATTGACACCTTTGTTATTAATCATGTGCTCTTACAGTGTAAATCATGTGAGCATC  
45 TTCAAAATTAGCTCTTCCGAGGGGAGAAGCAAAAGTCTCTCACTGTTCAGCCCTCTGA  
CTGTGGTCATAAATTCTATGGGACCATCCTCTTCAATGTACATGAAGCCCAAGTCTAAAGA  
GACACCTAAATTCGGATGACTTGGATGTCACCGACAAAAATTATATCCATGTCTATGGGGTG  
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCA  
GTAAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 374)

50

#### AOLFR202 sequences:

55 MEWENHTILVEFFLKLGLSGHPRLLELFFVLIFIMYVILLNGTLLILSILDPHLHTPMYFFLGNL  
SFLDICYTTTSPSTLVSLSERKTISLSCAVQMFLSLAMGTTECVLGLVMAFDRYVAICNPLR  
YPIIMSKDAVYVMAAGSWIIGAVNSAVQTVFVQLPFCRNNIINHFTCEILAVMKLACADISGN  
EFILLVTTTFLILPLLLIIVSYTLIILSIFKISSSEGRSKPSSCSARLTVTVTITFLMYMKPKSQ

ETLNSDDLDATDKLIFFYRVMTPMMNPLYSLRNKDVKEAVKHLRRKNFNK (SEQ ID NO: 375)

5 ATGGAATGGGAAAACACACCATCTTGGTGGAAATTTTCTGAAGGGACTTCTGGTCACC  
CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGGGTCACTCTCTGGGG  
AATGGTACTCTCATTTTTAATCAGCATCTTGGACCTCACCTTCACACCCCTATGTACTTCTT  
TCTGGGGAACTCTCTCTTCTTGGACATCTGTACACCAACCACTCTATTCCCTCCACGCTAG  
TGAGGCTTCTCTTCAGAAAGAAAGACCAATTCCTCTTCTGGCTGTGCAGTGCCAGATGTTCT  
10 CAGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCGTGATGGCCCTTGGACGCTAT  
GTGGCTATCTGCAACCTCTGAGATATCCCATCATCATGATGAAGATGGCTATGTACCCA  
TGGCAGCTGGGTCTCGATCATAGGAGCTGTCAATCTGCAGTACAAACAGTGTGTTGTGGT  
ACAATTGCCCTTCTGCGAGGAATAACATCATCAATCATTTCACCTGTGAAATCTTAGCTGTC  
ATGAAACTGGGCTGTGCTGACATCTCAGGCAATGAGTTCATCTGCTGTGACCAACACAT  
15 TGTTCCTATTGACACCTTTGTATTAAATTATGTCTTACACGTTAATCATTTTGAGCATC  
TTCAAAATTAAGCTCTTCGGAGGGGAGAAGCAAACTTCTCTACCTGCTCAGCTCGTCTGA  
CTGTGGTGATAACATCTGTGGGACCATCTTCTCATGTACATGAAGCCCAAGTCTCAAGA  
GACACTTAATTCAGATGACTTGGATGCCACTGACAACTTATATTCAATTTACAGGGTG  
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGGAGGCA  
GTAACACCACTACTGAGAGAAAAAATTTTAAACAAGTAA (SEQ ID NO: 376)

**AOLR203 sequences:**

5 MKRQNRQSCVVEFILLGFSNFPPELQVQLFGVFLVIYVVTLMGNAITVIIISLNQSLHVPYMLFLLN  
LVTVVEVSFAVITPEMLVVLSTEKTMSISFVGCAQMYFILLFGGTCEFLLGAMAYDRFAAICHPL  
NYPVIMNRGVFMKLVIFSWISGIMVATVQTWVFSPPFCGPNNEINHLCFETPPVLELVCA DTFLF  
25 EIYAFGTILVMPFLJLLSYRVLFAILKMPSTGRQKAFSTCASHLSTVLFYGTANMTYLV  
PKSGYSPETKKLISLAYTLLTPLLNP LIYSLRNSEMKRTLILKLRWKVILHTF (SEQ ID NO: 377)

30 ATGAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCTCTGGGCTTTTCTAACTTTC  
CTAGCTCCAGGTGCAGCTCTTTGGGGTTTTCCTAGTATTATGTGGTGACCCCTGATGGG  
AATAGCCATCAATACAGTCATCATCTTAAACAGACGCTCCACGTTCCCATGTACCTGT  
TCTCTCTGAACCTATCTGTGGTGAGGTGAGTTTCAGTGCACTATTACGCTGAAATGCT  
GGTGGTGCTCTCTACTGAGAAAATCATGATTTCTTTGTGGGCTGTTTGTGCAGATGAT  
35 TTCTCTCTCTTTTGGTGGGACTGAATGTTTCTCTCGGAGCGATGGCTTATGACCGATT  
TGCTGCAATTTGCCATCCTCTGAACCTACCCAGTGATTATGAACAGAGGGGTTTTATGAAA  
TTAGTAATATTCTCATGGATCTCAGGGATCATGGTGGCTACTGTGCAGTCACTGGGTAT  
TTAGTTTTCATTTTGTGGCCCAATGAAATTAATCATCTCTCTGTGAGACTCCCCGGTA  
CTAGAGCTTGTGTGCGAGACACCTCTTATTGAAATCTATGCCTTCACAGGCAACATTT  
40 GATTGTTATGGTTCCTTTCTTGTGATCTCTTGTCTTACATTGAGTTCTGTTTGCCATCT  
GAAGATGCCATCAACTACTGGGAGACAAAAGGCCTTTCCACCTGTGCCTCAGCTCACA  
TCTGTGACCCCTGTCTATGACCAAGCAATATGACTATTACACCAAACTTCGGCTACT  
ACCCGAAACCAAGAACTGATCTCATTGGCTTACACGTTGCTTACCCCTCTGCTCAATCCG  
CTCATCTATAGCTTACGAAACAGTGAGATGAAGAGGACTTGTATAAACTATGGCGAAGA  
AAAGTGATTTTACACACATTCTGA (SEQ ID NO: 378)

**AOLR204 sequences:**

45 MEKKKNVTEFILLGLTQNPIMEKVTFVVFLVLYMITLSGNLLIVVTITTSQALSSPMYFFLTHLSL  
IDTVYSSSAAPKLIVDSFQEKLIIFNGCMAQAYAEHIFGATEILLTVMACDCCYVAICPLNYTT  
IMSHSLCILLVAVAVGGFLHATIQILFTVWLPFCGPNVIGHFMDCLYPLLKVICDHTHGLFV  
VAVNSGIFCLLNFILVYVSVIIIISLKNNSLEGRCKALSTCISHIVVVLFPVPCIFVYLSRVTTLPI  
50 DKAVAFVFTVMVPLNPPVVTYLRNAEVKSAIRKLNRKKVTSNDN (SEQ ID NO: 379)

ATGGAGAAGAAAAAGAAATGTGACTGAATTCATTTAATAGGTCTTACACAGAACCCCAT  
ATGGAAGAAAGTCACGTTTGTAGTATTTTGGTCTTTACATGATAACACTTTCAGGCAAC  
55 TGCTCATTTGGTTACCAATTACCACAGCAGGCTCTGAGCTCCCCCATGTACTTCTCTCTG  
ACCCACCTTTCTTTGATAGACACAGTTTATCTTCTTTCAGCTCTCAAGTGTATTGTGGA  
TTCCTTTCAAGAGAAGAAAAATCATCTCCTTTAATGGGTGTATGGCTCAAGCCTATGCAGAA



5 CACATTTTGGTGCTACTGAGATCATCTGCTGACAGTGATGGCCTGTGACTGCTATGTGG  
 CACTCTGCAAACTCTGAACTACACAACCATTATGAGCCACAGCCTGTGCATTCTCTGGT  
 GGCAGTGGCCTGGGTGGGAGGATTTCTTCATGCAACTATTCAGATTCTCTTTACAGATGAT  
 CTGGCCCTCTGTGGCCCCAATGTCATAGGCCACTTCATGTGTGACTCTGTACCAATGTTAA  
 10 ACTTGTGTCATAGACACTCATACCTTGGTCTCTTGTGCTGTGAACAGTGGGTTATCT  
 GCTTATTAACACTCTCTATCTTGGTGGTATCCTATGTGATCATCTTGAGATCTTTAAAGAAC  
 AATAGCTTGGAGGGGAGGTGTAAGCCCTCTCCACCTGTAATTTCTACATCATAGTAGTTG  
 TCTTATTCCTTTGTGCCCTGTATATTGTGTATCTCGCGCTCAGTGACCACCTGTGCCCATTTGAT  
 AAAGCTGTTGCTGTATTTTATACATATGGTGGTCCCAATGTTAAATCCCGTGGTCTACACAC  
 TCAGAAATGCTGAGGTAAGTGAATAAGGAAGCTTTGGAGAAAAAAGTGACTTCAG  
 ATAATGATTAA (SEQ ID NO: 380)

**AOLFR205 sequences:**

15 MESENRTVIREFILLGLTQSQDIQLLVFVLVLIIFYIILPGNFIIFTIKSDPGLTAPLYFFLGNLAF  
 DASYSYTVAPRMLVDFLSAKKIISYRGCTQLFFLHFGGGEGLLLVMAFDRIYAIICRPLHYPT  
 VMNPRTCYAMMLLALWLWGGFVSHIIVLRLPFCGPNQLDNFFCDVDPQVVKLACTDTFVVEL  
 LMFVNSGLMTLLCFGLLASVAVILCRIRGSSSEAKNKAMSTCITHIVIFMFPGFIYTRPRA  
 FPADKVVSLFHTVIFPLLNPVIYTLRNOQEVKASMKKVFVFNKHA (SEQ ID NO: 381)

20 ATGGAAAGCGGAGAAGACAGAACAGTGATAAGAGAATTCATCCTCCTTGGTCTGACCCAGTCT  
 CAAGATATTCAGCTCCTGGTCTTTGTGCTAGTTTAAATATTTCTACTTCATCATCCTCCCTGG  
 AAATTTTCTCATTATTTTACCATAAAGTCAGACCCCTGGGCTCAGACGCCCTCTATTTCT  
 TTCTGGGCAACTATGGCCTTCTGGATGCATCTCCTACTCTTCACGTGTGGCTCCCGGATGTTG  
 GTGGACTTCTCTCTGCGAAGAAGATAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTT  
 25 TCTTGACATCTCCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTA  
 CATCGCCATCTCGCCGCCCTCTGCATATCCTACTGTCAAGCCCTAGAACCTGCTATGCA  
 ATGATGTTGGCTCTGTGGCTTGGGGGTTTGTCCACTCCAATTACAGAGTGGTCTCCTACTCT  
 CCGCTTGCCTTTTGTGGCCAAACCAGCTGGACAACCTCTTCTGTGATGTCCACAGGTC  
 ATCAAGCTGGCCTGCAACCGACACATTGTGGTGGAGCTCTGATGGTCTTCAACAGTGGCC  
 30 TGATGACACTCCTGTGCTTCTGGGGCTTCTGGCCTCCTATGCAGTCACTCTTTGTGCGATA  
 CGAGGGTCTTCTTCTGAGGCAAAAAACAAGGCCATGTCCACGTGCATCACCCATATCATGT  
 TTATATCTTCATGTTTGGACCTGGCATCTTCATACACGCGCCCTCAGGGCTTCCCA  
 GCTGACAAGGTGGTTTCTCTCTTCCACACAGTGATTTTCTCTTGTGTAATCCTGTCAITTA  
 TACCTTCCGAACACGGAAGTGAAGCTTCCATGAAAAAGGTGTTTAAATAGCACATAGC  
 35 CTGA (SEQ ID NO: 382)

**AOLFR206 sequences:**

40 MANRNNVTEFILLGLTENPKMQKIIFVVSFVIYNAMIGNVLIVVITASPRLSPMYFFLAYLSFI  
 DACYSSVNTPKLITDSLYENKTILFNGCMQTQVGEHFFRGVEVILLTVMAVDHYVAICKPLHYT  
 TIMKQHVCSLLVGVSGGLFHATIQILFICQLPFCGPNVIDHFMCPLYTLINLACTNHTLGLF  
 IAANSFICILNCLLLVSCVILYSLKTHSLEARHEALSTCVSHITVVILSFIPCFVYMRPPTL  
 PIDKAVAVFYTMITSMLNPLYTLRNAQMKNAIRKLCSRKAISVVK (SEQ ID NO: 383)

45 ATGGCGAATAGAAACAATGTGACAGAGTTTATCTATTGGGGCTTACAGAGAAATCCAAAA  
 ATGCAGAAAAATCATATTTGTGTGTTTCTGTCACTACATCAAGCCATGATAGGAAATG  
 TGCTCATTTGGTGCACCATCACTGCCAGCCCATCACTGAGATCCCCATGTACTTTTCTCTG  
 GCCTATCTCTCTTTATTTGATGCCTGCTATTCCTCTGTCAATACCCCTAAGCTGATCACAGA  
 TCACTCATGAAAAACAAGCATATCTTATTCAATGGATGTATGACTCAAGTCTTTGGAGAA  
 CATTTTTTCAGAGGCTGTGAGGTCATCCTACTACTGTAAATGGCCTATGACCACATGTGG  
 50 CCATCTGCAAGCCTTGGCACTATACCACCATCATGAAGCAGCATGTTTGTAGCCTGCTAGT  
 GGGAGTGTATGGGTAGGAGGCTTCTTCATGCAACCATACAGATCCTCTTCATCTGTCAA  
 TTACCTTTCTGTGGTCTAATGTATAGATCACTTTATGTGTGATCTACACTTGTATGATCAA  
 TCTGTGCTGCACATAATACCACACTCTAGGACTCTTCATTGCTGCCAACAGTGGGTTTCATAT  
 GCCTGTAAACTGTCTTGTCTCTGGTCTCCTCGGTGCTCTACCTGACTCTCTTAAAGACC  
 55 CACAGCTTAGAGGCAAGGCATGAAGCCCTCTCTACCTGTGCTCTACCATCATGACTGTGCA  
 TCTTATCCTTTATACCTGCATATTTGTGTACATGAGACCTCCAGCTACTTTACCCATTGAT

AAAGCAGTTGCTGTATTCTACACTATGATAACTTCTATGTTAAACCCCTTAATCTACACCTT  
GAGGAATGCTCAAATGAAAAATGCCATTAGGAAAATTGTGTAGTAGGAAAGCTATTTCAGG  
TGTCAAATAA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSTEFFVLVLSAHPKLQTVFFVLJLWMYLMILLGNGLVISVIFDLSHLHTPMYFFLCN  
LSFLDVCYTSSTVPLILASFLAYKKKVSFSGCMVQMFIISFAMGATECMILGTMALDRYVAICY  
LRYPVIMSKGAYVAMAGSWVTGLVDSVVQTAFAMQLPFCANNVIKHFVCEIILAILKLACADI  
SINVISMTGSNLIVLVIPLLVISISYIFIVATILRIPSTEGKHAFSTCSAHLTVVVIIFYGTIFFMYAKP  
10 ESKASVDSGNEIIEALISLFYGVMPMLNPLIYSLRNKDVKAAVKNILCRKNFSDGK (SEQ ID  
NO: 385)

ATGGAAAGGACCAACGATTCCACGTCGACAGAATTTTCTGCTAGGGCTTTCTGCCACC  
CAAAGCTCCAGACAGATTTTCTCGTCTCTAATTTTGTGGATGTACCTGATGATCCTGCTGGGA  
15 AATGGAGTCTCTATCTCAGTTATCATCTTTGATTCTCACCTGCACACCCCATGTATTTCTT  
CCTCTGTAATCTTTCTTCTCGACGTTTGTCTACACAAAGTCTCTGTGCCACTAATTTCTTG  
CCAGCTTTCTGGCAGTAAAGAAAAAGGTTTCTCTCTGGGTGTATGGTGCAAAATGTTTAT  
TCTTTTGGCATGGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGGTAT  
GTGGCCATCTGCTACCCACTGAGATACCTGTCTCATGAGCAAGGGTGCCATATGTGGCCA  
20 TGGCAGCTGGGTCTGGGTCACTGGGCTGTGGACTCAGTAGTGACAGACGTTTGGCAAT  
GCAGTTACCAATCTGTGCTAATAATGTCTAATAACATTTGTCTGTGAAATTTCTGGCTATCT  
TGAAACTGGCCTGTGCTGATATTTCAATCAATGTGATTAGTATGACAGGTCGAATCTGAT  
TGTTCTGGTTAATCTCATTTGTAGTAATTTCCATCTCTACATATTTATTTGTGCCACTATCT  
25 GAGGATTCCTTCCACTGAAGGAAAAACATAAGGCCCTTCTCCACTGCTCAGGCCCACTGACA  
GTGGTGATTATATCTTATGGAACCATCTTCTCATGTACGCAAAAGCCTGAGTCTAAAGCCT  
CTGTGATTACAGGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTCTATGGAGTGAT  
GACTCCCATGCTTAATCTCTCATCTATAGTCTGCGAAACAAGGATGTAAGGCTGCTGTCT  
AAAAACATCTGTGTAGGAAAAAATCTTTCTGATGGAAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIIFAVCLLMYLITLLGNIFLISITILDSHLHTPMYFLSNL  
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTEVCVLLPMMAYDRYVAICNP  
LRYPVIMNRRTCVQIAAGSWMTGCLTAMVEMMSVPLSLCGNSIINHFTCEILAILKLVCVDT  
LVQLIMLVSVLLPMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVVLFYGTALSMH  
35 LKPSAVDSQEIDKFMALVYAGQTPMLNPIIYSLRNKEVKVALKKLLIRNHFTAFISILK (SEQ  
ID NO: 387)

ATGTTCCCGGCAAAATTGGACATCTGTAAAGTATTTTCTTCTGGGATTTTCTCACTACCC  
CAAAGTTACAGGTGCATCATATTTGCGGTGTGCTGTGCTGATGTACCTGATCACCTTGTCTGGG  
40 AACTATTTTCTGATCTCATACCAATCTAGATTCCCACTGCACACCCCATGTACCTCTT  
CCTCAGCAATCTCTCTTTCTGGACATCTGGTACTCCTCTTCTGCCCTCTCTCCAAATGGCTGG  
CAAACTTTGTTTTCAGGAGAGAAACATAATTTCATTCTCAGGGTGCAGCACTCAGATGTACCT  
CTCCCTTGCCATGGGCTCCTCAGTGTGCTGCTGCTGCCATGATGGCATATGACCGGTAT  
GTGGCCATCTGCAACCCCTGAGATACCTGTCTCATGAATAGGAGAACTGTGTGCGA  
45 GTGCAGCTGGCTCTGGATGACAGGCTGTCTCACTGCCATGTGTGGAATGTATGTTCTGTGCT  
GCCACTGTCTCTGTGGTAATAGCATCATCAATCATTTCACCTGTGAAATTTCTGGCCATCT  
TGAAATTTGGTTTGTGTGGACACCTCCCTGGTGCAGTTAATCATGCTGGTGATCAGTGTACT  
TCTTCTCCCCATGCCAATGCTACTCATTTGTATCTCTTATGCATTTATCTCTCGCCAGTATTC  
TGAGAATCAGCTCAGTGAAGGTGGAAGTAAAGCCCTTTCAACGTGCACAGCCCACTGTA  
50 TGGTGGTGAATTTTGTCTATGGGACGGCTCTCTCCATGCACCTGAAAGCCCTCGCTGTAGA  
TTCACAGGAAATAGACAAATTTATGGGCTTTGGTGTATGCCGGACAAACCCCATGTGTGAAT  
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATTTGCTGATTA  
GAAATCATTTAATACTGCGCTTGCATTTCCATCTCTCAATAA (SEQ ID NO: 388)

**AOLFR209 sequences:**

- MDKINQTFVREFILLGLSGYPKLEIIFALILVMYVVLIGNVLIASILDSRLHMPMYFFLGNLS  
FLDICYTTSISPSTLVSLISKKRNSISFGCAVQMFFGFAMGSTECLLGMMAFDTRYVAICNPLRY  
PIIMNKVVYVLLTSVSWLSGGINSTVQTSLAMRWPCGNININHLCEILAVLKLACSDISVINV  
TLAVSNIAFLVLPPLVIFVFSYMFILYTLRTNSATGRHKAFTSCSAHLTVVIFYGITFFMYAKPKS  
QDLLGKDNLQATEGLVSMFYGVVTPMLNPIYSLRNKNDVKAIAKYLRSKAINQ (SEQ ID NO:  
389)
- 10 ATGGACAAGATAAACACGACAGATTGTGAGAGAATTCATTCTCTGGGACTCTCTGGTTACC  
CCAAACTTGAGATCATTCTTTGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATGGC  
AATGGTGTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTCACATGCCCATGTACTTCT  
CCTGGGCAACCTCTCTTTCTGGATATCTGCTATACAAACCTCTCCATTCCTCAACACTGG  
TGAGCTTAATCTCAAAGAAAAGAAACATTTCCTTCTCTGGATGTGCAGTGACAGATGTTCTT  
15 TGGGTTTGAATGGGGTCAACAGAATGTTTCCTCCTTGGCATGATGGCAATTTGATCGTTAT  
GTGGCCATCTGTAACTCTGAGATACCCCATCATCATGAACAAGGTGGTGTATGTACTGC  
TGACTTCTGTATCATGGCTTTCTGGTGGAAATCAATTCACACTGTGCAACATCACTTGGCAT  
GCGATGGGCTTTCTGTGGGAACAATAATTAATCATTCTTATGCGAGATCTTAGCTGTCC  
TAAAAATAGCTTGTCTGTATATCTGTCAATATTGTTACCTAGCAGTGTCAAAATATTGCT  
20 TTCTAGTTCTTCTCTGCTCGTGATTTTTTCTCTATATGTTTCATCTCTACACCATCTTG  
CGAACGAACCTCGGCCACAGGAAGACACAAGGCATTTTCTACATGCTCAGCTCACCTGACTG  
TGGTGTACATATTTATGGTACCATCTCTTTATGTATGCAAAACCTAAGTCCAGGACCTC  
CTTGGGAAGAACAACCTTGCAAGCTACAGAGGGGCTGTGTTCCATGTTTATGGGGTGTGTA  
CCCCCATGTTAAACCCCATATACTATAGCTTGAGAAAAAAGATGAAAAAGCTGCTATAAA  
25 ATATTGTCTGAGCAGGAAAGCTATTAAACAGTAA (SEQ ID NO: 390)

**AOLFR210 sequences:**

- MMGRNDTNVADFLITGLSDSEEVQMALFMLFLIYLITMLGNVMGLIIRLDLQLHTPMYFFL  
THLSFIDLSTVVPKTLANLLTSNYISFTGCFQMFVFLGTAECYLLSSMAHYDRIAACSP  
LHYTVIMPKRLCLALITGPYVIGFIDSVNVVMSRLHFCDNSPIHLCFCDTSPILALSCDTPDN  
TEMLIFLAGSTLMSVLITISASYVSLSTILKINSTSGKQKAFSTCVSHLLGVTFYGTMIFTYLPK  
RKSYSGLGRDQVAPVFTIVPMLNPLIYSLRNREVKNALIRVMQRQDSR (SEQ ID NO: 391)
- 30 ATGATGGGTAGAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTACAGC  
TCTGAAGAGGTCCAGATGGCTCTGTTTATGCTATTCTCTCATATACCTAATTAATCTATGCT  
GGGGAATGTGGGGATGCTATTGATAATCCGCTTGGACCTCCAGCTTCACACTCCCATGTAT  
TTTTCTCTTACTACCTGTCAATTTATGACCTCAGTTACTCAACTGTCTGTACACCTAAAAAC  
CTTAGCGCAACTTACTGACTTCCAATATTTCTCACGGGCTGTTTGGCCAGATGTCTT  
40 GTTTTGTCTCTTGGGACTGCTGAATGTTATCTTCTCTCAATGGCCTATGATCGCTAT  
GCAGCGATCTGCAGTCTCTACACTACACAGTTATTATGCCCAAAAGGCTCTGCCTCGCTC  
TCATCACTGGGCTTATGTGATTGGCTTATGGACTCCTTTGTCAATGTGGTTTCCATGAGC  
AGATTGCATTTCTGTGACTCAACATAATTCATCACTTTTCTGTGACACTTCCCCAATTT  
AGCTCTGCTCTGCATGACACAGACAACACTGAAATGCTGATATTCATTATCGCTGGTTCC  
ACCTGATGGTGTCCCTATCACAATATCTGCATCCTATGTGTCCATTTCTCTACCATCTCT  
45 GAAAATTAATTCACCTTCAGGAAAGCAGAAAGCTTTCTCACTTGGGCTCTCATCTCTTG  
GGAGTCAACCATCTTCTATGGAATATGATTTTACTTACTTAAAGCCAAAGAGCTTATT  
CCTTGGGAAGAGATCAAGTGGCTTCTGTGTTTTATCACTATTGTGATTCCTGCTGAATCC  
ACTCATTTATAGTCTTATGAAACAGAGAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG  
AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)
- 50

**AOLFR211 sequences:**

- MMGRNRNTNVADFLIMGLTLEEIQMALFMLFLIYLITMLGNVMGLIIRLDLQLHTPMYFFL  
THLSFIDLSTVVPKTLANLLTSNYISFTGCFQMFVFLGTAECYLLSSMAHYDRIAACSP  
LHYTVIMSKRLCLALITGPYVIGFIDSVNVVMSRLHFYDSNVIIHFFCDTSPILALSCDTPDN  
55 EILFIHVGSTLMSVLITISASYVHLITILKINSTSGKQKAFSTCVSHLLGVTFYSTLIFTYLPKRP  
SYSLGRDQVASVFTIVPMLNPLIYSLRNKEVKNVIRVMQRQDSR (SEQ ID NO: 393)

5 ATGATGGGTAGAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTTT  
 CTGAAGAGATCCAGATGGCTCTGTTTATGCTATTTCTCCTGATATACCTAATTACTATGCTG  
 GGGAAATGTGGGGATGATATTGATAATCCGCCCTGGACCTCCAGCTTCACACTCCCATGTATT  
 10 TTTTCTTACTCACTGTCACTTTTATGACCTCAGTTACTCAACTGTGTCACACCTAAAACC  
 TTAGCGAACTTACTGACTTCCAACATATATTCTCTTACGGGGTGCTTTGCCAGATGTTCTT  
 TTTTGCTTCTGGGTACTGCTGAATGTTACCTTCTCTCTCAATGGCCCATGATCGCTATG  
 CAGCGATCTGCAGTCTCTACACTACACAGTTATTATGTCCAAAAGGCTCTGCCTCGCTCT  
 CATCACTGGGCCCTTATGTGATTGGCTTTATAGACTCCTTTGTCAACGTGGTTTCCATGAGCA  
 GATTGCTATTCTACGACTCAAACGTAATTCATCACTTTTCTGTGACACTTCCCAATTTTA  
 GCTCTGTCTGCATCTGATACATAACAACACCGAAATCCTGATATTCATTATGTTGGTTCAC  
 CCGATGGTGTCCCTTTTACAATATCTGCATCTCATGTGTTACTTCTTTACCATCTGCA  
 15 AAATTAATTCACCTTCAGGAAAGCAGAAAGCTTCTCTACTTGCCTCTCTCATCTCTGGG  
 AGTCACCATCTTTTATAGCACTCTGATTTTACTTATTTAAACCAAGAAAGTCTTATCTCT  
 TGGGAAGAGATCAAGTGGCTTCTGTTTATATACTATTGTGATTCCCGTCTGAATCCACT  
 CATTATAGTCTTAGAAACAAAGAGGTGAAAAATGCTGTCTCAGAGTCATGACAGAGAAG  
 ACAGGACTCCAGGTAA (SEQ ID NO: 394)

#### AOLFR212 sequences:

20 MAGNNFTEVTVFVLSGFANHPQLQVSLFLMFLFIYLFVTLGNLGLTILRMSQLHTPMYFFLSN  
 LAFIDIFYSSVTNPKLVNFQSNRRSISFVGCFFVQMYFFVLVCCCECFLGSMAYNRYIAICNPL  
 LYSVMSQKVSMVLGVMPYVIGFTSSLSVWVVISSLAFCDSSINHFCDTALLALSACVDFTGT  
 EMVSVFLAGFTLLSSLLIITVYIIISAILRIQSAAGROKAFSTCASHLMATVIFYGSLIFTYLPQD  
 NTSSLTQAQVASVFYTVIPMLNPLIYSLRNKDKVNALLRVIHRKLF (SEQ ID NO: 395)

25 ATGGCTGGGCAACAATTTCACTGAGGTTACCGTCTTCATCCTCTCTGGATTGCAAATCACC  
 CTGAATTACAAGTCAGTCTTTTCTTGATGTTTCTCTTCATTTATCTATCACTGTTTGGGA  
 AACCTGGGACTGATCACGTTAATCAGAATGGATTCTCAGCTCAGCCCACTGATCACTTTT  
 30 TCTCGAGCAATTATGCAATTTATGACATATTTACTCCTCTACTGTAACACCTAAGGCAATG  
 GTGAATTTCCAATCAATCGGAGATCCATCTCCTTTGTGGCTGCTTTGTTCAAATGTACTT  
 TTTTGTGGATTGGTGTGTTGTGAGTGTTTCTCTGGGATCAATGGCCTACAATCGCTACA  
 TAGCAATCTGCAATCCCTTACTGTATTCAAGTGCATGTCCCAAAAAGTGCCAACCTGGCT  
 GGGAGTAATGCCATATGTGATAGGCTTCAAGCTCGCTGATATCTGTCTGGGTGATAAGC  
 35 AGTTTGGCGTCTGTGATTCCAGCATCAATCAATTTTTTGTGACACACAGCTCTTTAGC  
 ACTCTCCTGTGTAGATACATTCCGGCACAGAAATGGTGAGCTTGTCTTLAGPCTGGGATCACT  
 CTCTCTAGCTCTCTCCTTATCATCACAGTCACCTATATCATCATCTCAGCCATCCTGAG  
 GATCCAGTCAGCAGCAGGCAGGCAGAGGCCTCTCCACCTGCGCATCCCACTCATGGCT  
 GTAACATATCTTTATGGGTCTCTGATTTTCACTATTGCAACCTGATAACACATCATCGCT  
 40 GACCCAGGCGCAGGTGCACTCTGATTTCTATACGATTGTCACTTCCCATCTGCAATCCATC  
 ATCTACAGTCTGAGGAACAAAGATGTGAAAAATGCTCTTCTGAGAGTCATACATAGAAAA  
 CTTTTTCCATGA (SEQ ID NO: 396)

#### AOLFR213 sequences:

45 MNSLGLKLVSMILSAHVFCYSKFNCFGCTHSIPALGADPPGGMGLGNESSLMDFILLGFSDDHRL  
 EAYLVFVFFLYLLTLVGNFTIIHSYLDPLPHTPMYFFLSNLSLLDICTTSLAPQTLVNLQRPKK  
 TITYGGCVAQLYISLALGSTECILLADMALDRYIAVCKPLHYVVMNPRLCQQLALISSWLSGLA  
 SSLIHAFTFLQLPLCGNHRLDHFICEVPAKLLKACVDTTVNELVLFVSVFLVPPALISISYGF  
 TQAVLRIKSVEARHKAFTSCSSHLTVVIIFYGTHIYVYLQPSDSYAQDQKGFISLFYTMVPTPLNP  
 IITYTLRNKDMKEALRKLLSGKL (SEQ ID NO: 397)

50 ATGAATAGTTTGGGAAAGTTGGTCTCCATGATCTCTCAGCTCATGTGTTCTGTTATTCTAA  
 ATTTAATTGTTTGGATGTACCATTTCCATTCTGCTTAGGTGGGATCCCCCTGGAGGG  
 ATGGGATTTGGGCAATGAGAGTTCCTAATGGATTTCATCTCTAGGCTTCTCAGACCAAC  
 CTGCTCTGGAAGGCTGTTCTCTTTGATTTGTCTTTTCTCACTCCTGACCTGACCTTGTGGGA  
 55 AACTTCACATAATCATCTCATATCTGGAATCCCTCTTCATACCCCAATGTACTTTT  
 TCTCAGCAACCTCTCTTACTGGACATCTGCTTCACTACTAGCCTTGTCTCTCAGACCTAG

TTAACTTGGCAAAGACCAAAGAAGACGATCACTTACGGTGGTTGTGTGGCGCAACTCTATAT  
 TTCTCTGGCACTGGGCTCCACTGAATGTATCTCTTGGCTGACATGGCCTTGGATCGGTAC  
 ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCAGGCCTTGGCAACAGC  
 TGGCATCTATCTCTGGCTCAGTGGTTGGCTAGTTCCTAATCCATGCAACTTTTACCTTG  
 CAATTGGCTCTCTGTGGCAACCAAGCTAGGCTGGACCAATTTTATTTGCGAAGTACCAAGCTCTCT  
 CAAGTTGGCTTGTGTGGACACCACTGTCAATGAATTTGGTGCTTTTGTGTGTAGTGTCTGT  
 TTGTTGTCAATCCACAGCACTCATCTCCATCTCCATGGCTTCAAACTCAAGCTGTGCTG  
 AGGATCAAAATCAGTAGAGGCAAGGCATAAAGCCTTCAGCACCTGTCTCTCCACCTTACAG  
 TGGTGAATATATTCTATGGCACCAATACTACGTGTACCTGCAACCTAGTGACAGCATGTG  
 CCAGGACCAAGGAAGTTTATCTCCCTCTCTACACCATGGTGACCCCACTTTAAATCTCT  
 ATCATCTATACCTTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAAACTTCTCTCGGA  
 AAATTGTGA (SEQ ID NO: 398)

#### AOLFR214 sequences:

MDKSNSSVYSEFVLLGLCSSQKLQLFYFCFVSFLYTVIVLGNLLILTVSDTSLHSPMYFLLGN  
 LSFVDICQASFAPKMIADFLSAHETISFSGCIAFFIHLFTGGEMVLLVSMAYDRVVAICKPLY  
 YVVMNRRRTCTVLVMISWAVSLVHTLSQLSFTVNLPPFCGPNVDSFFCDLPRVTKLCLDYSIIE  
 ILIVVNSGILSLSTFSLVSSYIILVTVWLKSSAAMAKAFSTLASHIAVVLFFGPCIFYVWPFTIS  
 PLDKFLAIIFYTVTPVLPVNLPIIYTLNRDMKAAYRKIVNHYLRPRRISEMSLVVRTSFH (SEQ ID  
 NO: 399)

ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTTGTACTGTTGGGACTCTGTAGTTCTC  
 AAAAACTCCAGCTTTTCTATTTTGTGTCTCTCTGTGTGTATACAGTCATTGTGCTGGGA  
 AATCTTCTCATATTCTCCACAGTGACTTCTGATACCAAGCCTGCACCTCCCTATGTACTTTCT  
 CTGGGAAACCTTTCTCTTGTGACATTTGTCAGGCTTCTTTTGTACTACCCCTAAATGATTG  
 CAGATTTTCTGATGGACACGAGACCATATCTTTCAGTGGCTGCATAGCCCAAAATTTCTTT  
 ATTCACTTTTACTGGAGGGGAGATGGTGCTACTTGTTCGATGGCTATGACAGCTTCTCTT  
 TAGCCCTTGCAAAACCTTATACTATGTGGTCATCATGAGCCGAAGGACATGCACGTCTCT  
 GGTAATGATCTCTGGGCTGTGAGCTTGGTGACACATTAAGCCAGTTATCATTTTACTGTG  
 AACCTGCCTTTTGTGGACCTAAATGTAGTAGACAGCTTTTGTGTATCTTCTCGAGTCAC  
 CAAACTTGCTGCCTGGACTCTTACATCATTTGAAATATAATTGTGGTCAATAGTGGAAIT  
 CTTTCCCTAAGCACTTTCTCTCTCTTGGTCAGCTCCTACATCATTTCTTGTGTACAGTTTG  
 GCTCAAGTCTTCAGCTGCAATGGCAAAGGCATTTTCTACGCTGGCTTCCCATATTGACGTA  
 GTAATATATTCTTTGGACCTTGCACTCTTCACTATGTGTGGCCCTTACCATCTCTCCCTT  
 GGATAAATTTCTTGCCATATTTTACACTGTTTTCACCCCGTCTCAAACCCCATATTATTATA  
 CACTAAGGAATAGGGATATGAAGGCTGCCGTAAGGAAAATTTGTGAACCATTAACGTAGGC  
 CAAGGAGAATTTCTGAAATGTCACTAGTAGTGAGAACTTCTTGCATTAA (SEQ ID NO:  
 400)

#### AOLFR215 sequences:

MAHTNESMVSEFVLLGLSNSWGLQLFFFAIFSIVYTVSVLGNVLIIVISFDSLHNSPMYFLLSNL  
 SFIDICQSNFATPKMLVDFIERKTISFEGCMAQIFVLHVSFVGSEMMLLVAMAYDRFAICKPLH  
 YSTMNRRLCVIFVSISWAVGLVSHVSLAFTVLDLPFCGPNVDSFFCDLPLVIELACMDTYEM  
 EIMTLTNSGLISLSCFLALISYITILIGVRCRSSSGSSKALSTLAHTIVVILFFGPCIFYVWPFSRL  
 PVDKFLSVFYTVCTPLNPIIYSLRNEDVKAAMWKLNRNHHVNSWKN (SEQ ID NO: 401)

ATGGCTCACAAATGAATCGATGGTGTCTGAGTTTGTACTTTTGGGACTCTCTAATTCCT  
 GGGGACTTCAACTTTTCTTTTTCGCCATCTCTCTATAGTCTATGTGACATCAGTGCTAGGC  
 AATGTCTTAATATTGTGCATTATTTCTTTTGACTCCCATTTGAATCTCTATGTACTTCTTG  
 CTGAGTAATCTTTCTTCAATTGATATCTGTCAGTCTAACTTTGCCACCCCCAAGATGCTGTG  
 AGACTTTTATTTAGCGCGAAGACTATCTCCTTTGAGGGTTGCATGGCCAGATATTCTGTT  
 CTTCACAGTTTGTGTGGGAGTGAGATGATGTTGGCTTGAGCTATGGCATATGACAGATTTA  
 TAGCCATATGTAAGCCTCTGCATACAGTACAATTATGAACGGCAGGCTCTGTGTAATTTT  
 TGTGTCTATTCTGGGCGGTGGGCGTCTTCAATCTCTGTGAGCCACTTGGCTTTACAGTGG  
 ACCTGCCATTCTGTGGTCCCAATGAGGTGGATGATCTTTTGTGACCTTCCCTTGGTGATA  
 GAGCTGGCTTGCAATGGATACATATGAAATGGAAATTATGACCCTAACCGAACAGTGGCCTG

ATATCATGTAGCTGTTTCCTGGCTTAATTATTTCTACACCATCATTTTGATCGGTGTCCG  
ATGCAGGTCTCCAGTGGGTACCTAAGGCTCTTCTACATTAAGTCCACATCACAGTG  
GTCAATCTTTCTTCGGGCCCTTGCAATTAATTTCTATATGGCCTTTTACGACACTTCTGT  
GGACAAATTTCTTCTGTGTTCTACACTGTTGTACTCCCTGTTGAACCCCATCATCTACT  
5 TTTGAGGAATGAAGTGTAAAGCAGCCATGTGGAAGCTGAGAAACCATCATGTGAACT  
CCTGGA AAACTAG (SEQ ID NO: 402)

**AOLFR216 sequences:**

MDVGNKSTMSFEVLLGLSNSWELQMFFFMVFSLLYVATVMVGNLSLIVTVIVDPHLHSPMYFL  
10 TNL SIIDMSLASFATPKMITDYLTHGKTI SFDGCLTQIFFLHLFTGTEIILLMAMSFDRYIAICKPL  
HYASVISPVQCVVALVVASWIMGVMHMSMQVIFALTLPCGPGYEVDSFFCDLPVVFQACVDY  
VLGLFMISTSGIILSCHVILFNSYVIVLVTVKHHSSRGSSKALSTCTAHFIVVFLFFGPCFIYMW  
PLSFLTDKILSVFYTIFTPTLNPHIYTLRNQEVKIAMRKLKNRFLNFKAMP (SEQ ID NO: 403)

15 ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTTGTTTTGCTGGGGCTCTCTAATTCCT  
GGGAACACTACAGATGTTTTCTTTATGGTGTTTTCATTGCTTTATGTGGCAACAATGGTGGG  
TAACAGCTCCATAGTACATCACAGTTATAGTGGACCCCTACCTACACTCTCCTATGATTTTCC  
TGTATACCAATCTTTCAATCATTGATATGTCCTTCTGCTCTTCGCGCACCCCAAGATGATT  
ACAGATTACCTAACAGGTACAAAACCATCTCTTTTGATGGCTGCTTACCAGATATTCT  
20 TTCTCCACTTTTCACTGGAACTGAGATCACTTACCTACGAGCCATGCTTTTGATAGGTAT  
ATTGCAATATGCAAGCCCTGCACTATGCTTGTGCTATAGTCCCCAGTGTGTGTGCTCT  
CTGGTGGCTTCTGGAATTATGGGAGTTATGATCAATGAGTCAAGTCAATTTGCGCCT  
ACGTTACCATCTGTGGTCCCTATGAGGTAGACAGCTTTTCTGTGACCTTCTGTGGTGT  
CCAGTTGGCTTGTGTGGATACTATGTTCTGGGCTCTTTATGATCTCAACAAGTGGCATA  
25 ATTGCGTGTGCTGTTTATTTATTTATTTAAATTCATATGTTATTGCTGCTGTTACTGTGAA  
GCATCATCTTCCAGGAGTATCTAAGGCCCTTTCTACTTGTACAGACTCATTTCACTTGTG  
TCCTTGTGTTCTTTGGGCCATGCATCTTCACTATCATGTGGCCACTAAGCAGCTTTCTCACA  
GACAAGATTCTGTCTGTGTTTATACCATCTTTACTCCACTCTGAACCAATAATCTATAC  
TITGAGGAATCAAGAAGTAAAGATAGCCATGAGGAAACTGAAAAATAGGTTTCTAAATTT  
30 TAATAAGCAATGCCTTCATAG (SEQ ID NO: 404)

**AOLFR217 sequences:**

MLESFQKSEQMAWSNQSAVTEFILRGLSSSELEQIFYFLFFSIVYAAVTLGNLLIVVTIASEPHLH  
SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAI SFEQCMTQMFFLHLLGGAIEVLLISMSFD  
35 RYVAICKPLHYLTIMSRMCMVGLVILSWIVGIFHALSQLAFTYNLPCGPNVDSFFCDLPV  
LACVDYTLGVFMISTSGMIALVCFILLVISYTHLVTVRQRSSGSSKALSTCSAHFTVVTLFFGP  
CTFIYVWPFNTFNDPKVLSVFYTIYTPLLNPVIYTVRNKDVKYSMRKLSSHIFKSRKTDHPT  
(SEQ ID NO: 405)

40 ATGCTAGAGTCTCTCCAGAAATCAGAGCAAAATGGCCTGGAGCAATCAGTCTGCGGTAACC  
GAATTCATACTACGGGGTCTGTCCAGTTCTTTAGAACTCCAGATTTTCTACTTCTGTTT  
CCCATATGCTATGTCAGCAGCTGTGCTGGGGAACCTTCTATTGTGTCACCATTGATCA  
GAGCCACACCTTCATTTCCCTACGTACTTTCTGCTGGGCAATCTCTCCTTCAATTGACATGT  
CCTGGCCATATTGCCACCCCAAAATGATTGCAGACTTCTTAGAGAACACAAAGCCATC  
45 TCTTTTGAAGGCTGCATGACCAAGATGTTCTTCTCTACATCTCTTAGGGGGTGTGAGATTG  
TACTGCTGATCTCCATGTCTTTTGATAGGTACGTGGCTATCTGAAGCTCTACATTACCTA  
ACAATCATGAGCCGAAGAAATGTGTGTGGCTGTGTACTTTCTGGAATTGTCGGCATCT  
TCCATGCTCTGAGTCAGTTAGCAATTACAGTGAATCTGCCCTTCTGTGGACCCAATGAAGT  
AGACAGTTCTTTTGTGACCTCCCTTTGGTGATTAATCTTGTGTGTGACACATATATTC  
50 TGGGGGTGTTACATGATCTCAACCAAGTGGCATGATGCCCCGTGTGCTTCATCTCTTGTG  
GATCTCTTACACTATCATCTGGTCACCGTTCCGCGAGCGTTCCCTCTGGTGGATCTCCAAA  
GCCCTTCCACGTGACGTGCCCACTTTACTGTGTGACCCCTTTCTTTGGCCCATGCATTT  
CATTTATGTGTGGCTTTTCAAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA  
TATACCTCCCTTCTGAATCCAGTGATCTATACCGTTAGGAATAAAGATGTCAAGTATG  
55 CATGAGGAACTAAGCAGCCATATCTTTAAATCTAGGAAGACTGATCATACTCCTTAA  
(SEQ ID NO: 406)

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#### AOLFR218 sequences:

METANYTKVTEFVLITLQTSREVQLVLFVIFLSFYLFILPGNLIICTIRLDPHLTSPMYFLLANLA  
LLDIWVSSITAPKMLIDIFFVERKIIISFGGCIQLFLHFVGAASEMFLIVMAYDRYAAICRPLHYA  
5 TMMNRRLCCILVALSWMGGFHSIIQVALIVRLPFCGPNELDSYFCDDITQVVRICAMTFPEELVM  
ICSSGLISVVCFAILLMSYAFLLALLKKHSGSDENTNRAMSTCYSHITIVLVMFGPSTIYIARPPD  
SFSLDKVVSVFHTVIFPLLNPIIYTLRNKEVKAAMRKVVTKYILCEEK (SEQ ID NO: 407)

ATGGAACCTGCAAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC  
GGGAGGTCACCAACTAGTCTATTTGTTATATTTCTATCCTCTTATTTGTTCTATCCTACCAGGA  
10 AATATCCTTATCATTTGACCATCAGGCTAGACCCTCATCTGACTTCTCTATGTATTTCTCT  
GTTGGCTAATCTGGCCCTCTTGATATTGGTACTCTTCCATTACAGCCCTCAAAATGCTCA  
TAGACTCTCTTGTGGAGGAGGAATAATTTCCCTTTGGTGGATGCATTGCACAGCTCTCTCT  
CTTACACTTTGTTGGGGCTTCGGAGATGTTCTTGCTCATAGTGATGGCCTATGACCCTAT  
15 GCTGCTATCTGCCGACCCTCCACTATGCTACCATCATGAATGCAGCTCTCTGCTGTATCCTT  
GGTGGCTCTCTCTGGATGGGGGGCTTCATTCTATAATACAGGTGGCTCTCATTTGTT  
CGACTTCTCTTCTGTGGGCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTG  
TCGGGATTGCTGTGCCAACACCTTCCACAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCT  
GATCTCTGTGGTGTGTTCAATTGCTCTGTTAATGTCCTATGCCTTCTCTGGCCTTGCTCA  
20 AGAAACATTCAGGCTCAGATGAGAATACCAACAGGGCCATGTCACCTGCTATTCCACAT  
TACCATTGTTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCAT  
TTTCCCTAGATAAAGTGGTGTCTGTGTTTCACTGTAATATTTCCCTTTACTTAATCCCAT  
ATTACCATTTGAGAAACAAGGAAGTAAAGGCACCCATGAGGAAGGTGGTCAACCAATAT  
ATTTTGTGTGAAGAGAAGTGA (SEQ ID NO: 408).

#### AOLFR219 sequences:

MLTSLDLCSFIQVAEIKSLPKSMNETNHSRVTEFVLLGLSSRELQPFLLTFSLLYLAILLGNF  
LILITVTSRSLHTPMYFLLANLSFIDVCVASFATPKMIADFLVERKTSIFDACLQIFFVHLFTGS  
EMVLLVSMAYDRYVAICKPLHYMTVMSRRYCVVLVLISWVFGIHTTSLQAFITVNLPCGPN  
30 KVDSEFCDLPLVTKLSLCDITYVVSLLIVADSLVLSFLLVSVYTVILTVNRSSASMAKAR  
SLTIAHITVVLFRGCPFIYVWPFSSYSVDKVLAVFYTIFLILNPVIYTLRNKEVKAAMSKLKS  
RYLKPSQVSVVIRNVLFLETK (SEQ ID NO: 409).

ATGCTCACTTCATTAACTGATCTCTGTTTCTCTCTTATTCAGGTAGCTGAAATTAAGTCCCT  
TCCAAAATCGATGAATGAGACAAATCATTTCTCGGGTGACAGAATTTGTGTGCTGGGACTG  
35 TCAAGTTCAAGGGAGCTCCAACCTTTCTGTTTCTTACATTTTCACTACTTTATAGCAAT  
TCTGTTGGGCAACTTTCTCATCATCTCACTGTGACCTCAGATTCCCGCCTTACACACCCCA  
TGTACTTTCTGTTGCAAAACCTGTCAATTATAGACGTATGTGTGCTCTTTTGCTACCCCT  
AAAATGATTGCGAGACTTTCTGGTTGAGCGCAAGACTATTCTTTGATGCTGCTGCTGCCCC  
40 AGATTTTCTGTTCTATCTCTTCACTGGCAGTGAAATGGTGCTCCTAGTTCCATGGCCTAT  
GACCGTTATGTTGCTATATGCAAACTCTCCACTACATGACAGTATGAGCGCTGCTGTAT  
GTGTTGTGCTCGTCCCTCATTTCAATGGTTTGTGGGCTTCACTCACTACCAGCAGTGTGGCA  
TTCACTGTAAATCTGCACTTTTGTGGTCTAATAAGGTAGACAGTTTCTTGTGACCTTCT  
TCTAGTGACCAAGAACTAGCCTGCATAGACACTTATGTTGTGACGCTTACTAATAGTGCAGAT  
45 AGTGCGTTCTTCTTCTCTGAGTTCCTTTCTCCTCTTGTTGTGCTCCTACACTGTAATACTTGT  
ACAGTTAGGAATCGCTCCTCTGCAAGCATGGCGAAGGCCGCTCCACATTGACTGCTCACA  
TCACTGTGGTCACTTTATCTTTGGACCATGCAATTTTCACTATGTTGTGGCCCTTCAAGCAT  
TACTCAGTTGACAAAGTCTTGTGCTATTCTACACCATCTTACGCTTATTTTAAACCTGT  
AATCTACAGCTAAGAAACAAGAAGTGAAGGCAGCTATGTCAAACTGAAGAGTCGGTA  
50 TCTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTCTTTTCTGAGAAACAAGTAA  
(SEQ ID NO: 410).

#### AOLFR220 sequences:

MKQYSVGNQHSNYSLLFPFLCSQMTQLTASGNQTMVTEFLFSMPHAHRGGLLFIPLLIIYG  
FILTGNLMFVIVQYGMALHTPLYYFISVLSFIEICYTTTTPKMLSCISEQKSISVAGCLLQMYFF  
55 HSLGITESCVLTAIDAIRYAIACNPLRYPTIMPKLCLQLTVGSCFCGFLVLPEIAWISTLPFCGS

NQIHQIFCDFTPVLSLACTDTFLVVVIDAIHAAEIVASFVLVIALSYIRIIVILGMHSAEGHHKAFST  
CAAHLAVFLFLFGSVAVMYLRFSATYSVFWDITAVITFVLAPFFNPIIYSLKNKMDKEAIGRLF  
HYQKRAGWAGK (SEQ ID NO: 411).

5 ATGAAGCAATATTCAGTGGGTAATCAACATTCGAATATAGGAGTCTCTTGTTCCTTTTCT  
GTGTTFCAGATGACACAGTTGACGGCCAGTGGGAATCAGACAAATGGTGACTGAGTTCCT  
CTCTCTATGTTCCCGCATGCGCAGAGAGGTGGCCCTCTTATTTCTTATTCCTCTGCTCTCA  
TCTACGGAATTTCTAACTGGAAACCTAATAATGTCAATGTCAATCCAGTGGGCATGGC  
10 CCTGACACACCCCTTTGTATTTCTTATCAGTGTCTCTCTCTCTGGAGATCTGCTATACCA  
CAACCACCATCCCCAAGATGTCTGTCTGCTAATCAGTGAGCAGGAAGCAATTTCCGTGGC  
TGGCTGCCTCTCGAGATGTACTTTTCCACTCACTTGGTATCAGAAAAGCTGTGTCTGT  
ACAGCAATGGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAAACATCA  
TGATTCCCAAACTTGTATCCAGCTGACAGITGGATCTGTCTTTGTGGCTCTCTCTGTGT  
15 CTTCCTGAGATTGCAATGGATTTCACACTTGCCTTTCTGTGGCTCCAAACAGATCCACCAGAT  
ATTCGTGATTTCACACCTGTGCTGAGCTTGGCCTGCACAGATACATTCCTAGTGGTCATT  
GTGGAATGCCATCCATGCAGCGGAAATGTAGCCTCTCTCTGGTCATTGCTCTATCTCTACA  
TCCGGATTATTATAGTGATTCTGGGAATGCACCTACGCTGAAGGTATCAACAAGGCCCTTTTC  
CACCTGTGCTGCTCACTGTGCTGTCTTGTCTATTTTGTGGCAGTGTGGCTGTCTATGTATT  
TGAGATTCTCAGCCACTACTCAGTGTTTTGGGACACAGCAATGTCTGTCACTTTTGTATTCT  
20 TGTGCTCTCTTTTTCACCCCATCATCTATAGCCTGAAAAACAGGAAGAGGCTA  
TTGGAAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGGCTGGGAAATAG (SEQ ID NO:  
412).

#### AOLFR221 sequences:

25 MRNLSGGHVEEFVLVGFPTTPPLQLLLFVLFFAIYLLTLENALIVFTIWLAPSLHRPMYFFLGH  
LSLEFLWYINVTIPRLAAFLTQDGRVSYVGCMTQLYFFIALACTECVLLAVMAYDRYLAI  
LLYSLMPPSSLATRLAAASWGSWGSMMKLLPISQLSYCGPNIIHFFCDISPLLNTCSDKEQA  
ELVDFFLLALVMILLPLLAUVSSYTAIIAILRIPTSRGRHKAFSTCAAHLAUVVIYSSYSLFTYAR  
PRAMYTENHNKIISVLYTIIVFFNPAIYCLRNKEVKEAFRKTVMGRCHYPRDVQD (SEQ ID  
30 NO: 413).

ATGAGAAATTTGAGTGGAGGCCATGTCGAGGAGTGTGTCTTGGTGGGTTCCTCCTACCACGC  
CTCCCCTCAGCTGCTCCTCTTGTCTTTTITGCAATTTACCTCTGACATTTGTTGGAGA  
ATGCACTTATTTGCTTCACAATATGGCTTGTCTCAAGCCTTCATCGTCCATGTACTTTTTC  
35 CTGGCCATCTCTCTTCTGGAGCTATGGTACATCAATGTCAACCTTCTCGGCTCTTGGC  
AGCCTTTCTTACCAGGATGGTAGAGTCTCTACGTAGGTGTGATGACCACTGTACTTCT  
TTTATTGCTTACCGGTGTACTGAAATGTGTGCTGTGGCAGTTATGGCTATGATCGCTACCT  
GGCCATCTGTGGACCCCTCTCTTACCTAGTCTCATGCTTCCAGTCTGGCCACTCGCCTTG  
CTGCTGCTCTTGGGGCAGTGGCTTCTTACGTCCATGATGAAGCTCTTTTATTTCCTCAA  
40 TTGTCCTACTGTGGGACCCAACTATCAACCACTTTTCTGTGATATTTCCCCACTACTCAA  
CCTCACTGTCTTGACAAGGAGCAAGCAGAGCTAGTAGACTTCTCTTGGCCCTGGTGATGAT  
ATTCTACTCCCTCTATTGGCTGTGTTTTCATCATACACTGCCATCATTCGAGCCATCTCGAG  
GATCCCTACGTCCAGGGGACGCCACAAGCCTTTTCCACTGTGCGCGTCTATCTGGCAGTG  
GTGTGTATCTACTACTCTCCACTCTCTTCACTGTGACGCGCCGGGCCATGTACACCTT  
45 CACTACCAACAAGATTATCTGTGTCTTACACTATCATTTGATCACTTCTTCAACCCAGCCA  
TCTACTCGCTGAGGAACAAGGAGGTGAAGAGGCTCAGGAAGACAGTGATGGGCAGAT  
GTCATATCTAGGATGTTTCAGGACTGA (SEQ ID NO: 414).

#### AOLFR222 sequences:

50 MGQTNVTSWRDFVFLGFSSSGELQLLLFALFLSLYVLTLSNVFIIAIRLDSHLHTPMYFLFLSFL  
SFSETCYTLGIHPRMLSLGAGGDQAIYSVGCQAQMFFSASWACTNCFLLAAMGFDYRVIAICAPL  
HYASHMNPFLCAQVITISFLTGYLFGMLTVIHLVHLSFSSSHEIQHHYCFDTPPVVLSLACGDTGPS  
ELRIFLSLVLLVSFFFTTISYAYILAILRIPSAEGQKKAFTCASHLTVVIHGYCASVYLRPK  
ASYSLERDQLIAMTYTVVTPLLNPVYSRLRTRAIQTALRNAFRGRLLGK (SEQ ID NO: 415).



ATGGGGCAGACCAACGTAACCTCCTGGAGGGGATTTTGTCTTCTGGGCTTCTCCAGTTCTG  
GGGAGTTGCAGCTCCTTCTCTTTGCTTGTTCCTCTCTGTATCTAGTCACTCTGACCAGC  
AATGTCTTCATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCATGTACCTCTT  
CCTTCTCCTCTCTATCCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAAATGCTCT  
5 CTGGCTGGGCGGGGACCAGGCTATCTCCTATGTGGGCTGTGGTGCCCGAGATGTTCTT  
TTCTGCCTCATGGGCTGTACTAACTGCTTCTCTGGCTGCCATGGGCTTTGACAGATAGT  
TGGCCATCTGTGCTCCACTCCACTGCCAGCCACATGAATCCTACCTCTGTGCCAGATG  
GGTCATTACITCCTTCTGACTGGATACCTCTTTGGAGCTGGGAATGACACTAGTATTTTCC  
ACCTCTCATTTCTGCAGCTCCCATGAAATCCAGCACTTTTTTTGTGACACGCCCACTGTGCTG  
10 AGCTGAGCTGTGGAGATACAGGCCCGAGTGAGCTGAGGATCTTTATCCTCAGTCTTTTGG  
TCCTCTTGGTCTCCTTCTTCTTCATCACCATCTCCTACGCCTACATCTTGGCAGCAATACTG  
AGGATCCCTCTGTGAGGGGAGAAAGGCGCTTCTCCTCTGTGCCTCGCACCTTACAG  
TGGTCAITATTCATTATGGCTGTGCTTCTTGTGTACCTGAGGCCAAAGCCAGCTACTCT  
CTTGAGAGAGATCAGCTTATTGCCATGACCTATACGTGATGACCCCTCTCTTAATCCCA  
15 TTGTTTATAGTCTAAGGACTAGGCTATACAGACAGCTCTGAGGAATGCTTTTCAAGGGAG  
ATTGCTGGGTAAGGATGA (SEQ ID NO: 416).

**AOLFR223 sequences:**

MEAA NESSEGISFVLLGLTSPGQQRPLFVLFLLLYVASLLGNLIVAAIQASPALHAPMYFLLA  
20 HLSFADLCFASVTVPKMLANLHSDHSLAGCLTQMYFFALGVDTSCLLAAMAYDCYVAIR  
HPLPYATRMSRAMCAALVGMAWLVSHVSHLLYILLMARLSFCASHGVPVPHFFCDHQLRLRSC  
SDTHHQLLIFTGAAVYVTFLLILASYGAIAAAVLQLPSASGRLRAVSTCGSHLAVVSLFYGT  
VIAVYFQATSRREAWEWRVATVMYTVTPMLNPIIYSLWNRDVQGALRALLIGRRISASDS  
(SEQ ID NO: 417).

ATGGAGGGCTGCCAATGAGTCTTCAAGGGGAATCTCATTCGTTTTATTGGGACTGACAACA  
GTCTGGACAGCAGCGGCTCTCTTTGTGCTGTTCTTGCTCTGTATGTGGCCAGCTCCTG  
GGTAATGGACTCATGTGGCTGCCATCCAGGCCAGTCCAGCCCTTCATGCACCCATGTACT  
TCTGTGTCGCCCACTGCTCTTTGTGACCTCTGTTTTCGCTCCGTCATCTGTGCCCAAGAT  
30 TTGGCCAACTTTGTGGCCATGACCACTCCATCTCGCTGGCTGGCTGCTGACCCAAATGT  
ACTTCTCTTTTGGCCCTGGGGGTAACGTATAGCTGTCTTCTGGCGGCCATGGCCCTATGACTG  
CTACGTGGCCATCCGGCACCCCTCCCTATGCCACAGGATGTCCCGGGCATGTGGCGCA  
GCCCTGTGGGAATGGCATGGCTGGTGTCCACAGTCCACTCCCTCTGTATATCTGCTCA  
TGGCTCGCTTGTCTTCTGTGCTTCCACCAAGTGCCCACTTCTCTGTGACACCAAGCCT  
35 CTCTTAAGGCTCTGTGCTCTGACACCCACCACATCCAGCTGTCTCATCTTACCGAGGGCG  
CGCGAGTGGTGTCACTCCCTTCTGCTCATCTCGCTCCTATGGGCCATCGCAGCTGC  
CCTGCTCCAGCTGCCCTCAGCCTCTGGGAGGCTCCGGGCTGTGTCCACTGTGGCTCCAC  
CTGGCTGTGGTGAGCCTCTTCTATGGGACAGTCACTGCAGTCTACTTCCAGGCCACATCCC  
GACGCGAGGCAGAGTGGGGCGGTGGGCCACTGTCACTGTACACTGTAGTACACCCCATCG  
40 TGAACCCCATCATCTACAGCCTCTGGAATCGCGATGTACAGGGGCGCATCCGAGCCCTCT  
CATTGGGCGAAGGATCTCAGCTAGTGACTCTGA (SEQ ID NO: 418).

**AOLFR224 sequences:**

MGSFNTSFEDGFLVWQLEPILVFIFIFYSLTFLFNGTIIIALSWLDRLHTPMYFFLSHLSL  
45 LDLCFTTSTVPPQLLNLCVDPRTTRGGCVAQLFIYALGISTECVLLVVMADFRAAVCRPLHY  
MAMHHPHLQTLAIAWSWAGFVNSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGT  
EAKMFVARVIVVAVPAALILGSYVHIAHVLRVKSTAGRRKAFGTGSHLLVFLFYGSAIYT  
YLQSIHNYSEREGKFVAFYTIITPILNPLYITLRNKDVGKALWKVLWRGRSD (SEQ ID NO:  
419).

ATGGGAAGTTTCAACACCAAGTTTTGAAGATGGCTTCATTTTGGTGGGATTCTCAGATIGGC  
CGCAACTGGAGGCCATCTGTTTGTCTTTATTTTATTTTCTACTCCCTAACTCTCTTGGC  
AACACCATCATCATCTCTCTCCTGGCTAGACCTTCGGCTGCACACACATGTACTCTTCT  
TCTCTCTCATCTGTCCCTCTGGACCTCTGCTTCAACACAGCAGCGTGCCGCACTCTGA  
55 TCAACCTTTGGCGGGTGGACCGCACCATCAACCGTGGAGGGTGTGTGGCTCAGCTCTTCAT  
CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCTGGTGGTATGGGCTTTGACCGCTAT

5 GCTGCTGTCTGTGCTCCACTCCACTACATGCCCATCATGCACCCCATCTCTGCGCAACCCCT  
GGCTATCGCCTCTCTGGGGTGC GG GTTCGTGAACCTCTCTGATCCAGACAGGTCTCGCAATG  
GCCATGCTCTCTGTGGCCATCGACTGAATCACTTCTCTGTGAGAGTGCTGTGATTTCTGAA  
GTTGGCTTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCGAGTGCATAGT  
10 CGTGCTGTCTCTGCGACCTTATTCTAGGCTTCTATGTGCACATTTGCTCATGCACTGGCTG  
AGGGTGAAGTCAACGGCTGGGCGCAGAAAGGCTTTTGGGACTTGTGGGTCCCACTCTCA  
TGATTTTCTCTTTTATGGCTCAGCCATCTACACATATCTCCAATCCATCCACAATATTTC  
TGAGCGTGAGGGAAAAATTTGTTGCCCTTTTATATACTATAATTACCCCACTTCTCAATCCTC  
TCATTTATACATAAGAAAAACAAGGACGTGAAGGGGGCTCTGTGGAAAGTACTATGGAGGG  
CGAGGGACTCAGGTAG (SEQ ID NO: 420).

**AOLFR225 sequences:**

15 MENYNQTSDFILLGLFPSSIIDLFFILIVFIFLMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID  
LNYISTIVPKMASDFLHGNKSISFTGCIQSFFFLALGGAEALLASMAFYDRYIAJCFPLHYLIRM  
SKRVCLMITSWIGGSINACHTVYVHLHPYCRSRAINHFCDVPAMVTLACMDTWVYEGTV  
FLSATILFVFPFIGISCSYQVLFVYHMKSAEGRKKAYLTCSTHLTVVTFYAPFVYTYLPRPS  
LRSPTEDEKVLAVFYTILTPMLNPIIYSLRNKEVMGALTRVSQRJCSVKM (SEQ ID NO: 421).

20 ATGGAATAATTACAATCAACATCAACTGATTTTCATCTTATTGGGGCTGTTTCCACCACAA  
TAATTGACCTTTCTTCTTCATCTTCTCATTGTTTTCATTTTCCGATGGCTCTAATGTGAAAC  
TGTTCCATGATTCTTCTCATCTCTCTGACACCCCATCTCCACACACCCATGTATTTCTACTG  
AGTCAGCTCTCCCTCATTTGACCTAAATACATCTCCACCACTTGTCTCTAAGATGGCATCTGA  
25 TTTTCTGCGATGGAAACAAGTCTATCTCTCTCACTGGGTGGGATTCAGAGTTTCTTCTCT  
TGCCATTAGGAGGTGACAGAACACTACTTTTGGCATCTATGGCCATATGATCGTTACATGCT  
TATTGCTTTCTCTCTCCACTATCTCATCCGATGAGCAAAAGAGTGTGTGCTGATGATA  
ACAGGGCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATATGTACTCCATA  
TGCTTATTGCGGATCCAGGGCCATCAATCTTCTCTGTGATGTCCAGCAATGGTGACT  
CTGGCCTGCATGGAACCTGGGTCTATGAGGGCACAGTGTTTTGTAGTGCCACCATCTTTC  
30 TCGTGTTCCTCTCATTGGTATTTTCATGTTCTTATGGCCAGGTCTCTTGTCTGTCTACAC  
ATGAAATCTGCAGAAAGGAGGAAGAAAGCCCTATTGTACCTGCAGCACCCACCTCACTGTA  
GTAACCTTCTACTATGCACCTTTTGTCTACACTTATCTACGTCCAAAGATCCCTGCGATCTCC  
AACAGAGGACAAGGTTCTGGCTGTCTTCTACACCATCTCACCCCAATGCTCAACCCCATC  
ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGGCCCTGACACGAGTGAGTGACGAGAATC  
35 TGCTCTGTGAAAATGTAG (SEQ ID NO: 422).

**AOLFR226 sequences:**

40 MEWRNHSGRVSEFVLLGFPAPAPLQVLLFALLLAYVVLVTENTLIIMAIRNHSTLHKPMYFLL  
ANMSFLEIYVYVVTIPKMLAGFVGSKQDHGQLISFEGCMTQLYFFLGLGCTECVLLAVMAYD  
RYMAICYPLHYPIVVSRLCVQMAAGSWAGGFISMVKVFLISGLSYCGPNINHFCDVSPLL  
NLSDTMSAEALFDIFILAILLGPLSVTGSASYVAITGAVMHISSAAGRYKAFSTCASHLTVIIF  
YASIFIYARPKALSAFDITNKLVSPLYAVIVPPLNPIIYCLRNQEVKRALCCTLHLYQHQPDP  
KKASRNV (SEQ ID NO: 423).

45 ATGGAGTGGCGGAACCATAGTGGGAGAGTGAGTGAGTTTGTGTGTGGGCTTCCCTGCT  
CCTGGCCACTACAGGTACTATTGTTGCCCTTTGTGCTGCTGGCCTATGTTGTTGGTGCTGAC  
TGAGAACACACTCATATTATGGCAATTAGGAACCACTTCACTCCACAAACCCATGTAC  
TTTTTCTAGCTAAATATGCTTTCTGGAGATCTGGTATGTCACCTGCTACTATTCACCAAGAT  
GCTGTGCTGGCTTTGTTGGATCCAAACAGGATCATGGACAGCTAATCTCTCTTGAAGGATGC  
ATGACACAGCTCTACTTTTCTTGGCTTGGGCTGCACTGAGTGTGTCCTTCTCGCTGTAT  
50 GGCTATGATCGCTATATGGCCATCTGCTATCCTCTCCACTACCCAGTCAATTGTCAGTGGCC  
GGCTGTGTGTGCAGATGGCTGCTGGCTCTTGGGCTGGAGGTTTGGCATCTCCATGGTCAA  
AGTTTTTCTTATTCTGGCCTCTCTTACTGTGGCCCAACATCATCAACCACTTTTCTGTG  
ATGTTCTCTCAATGTCTAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTCT  
ATCTGGGCATTTTATCTTCTTCAAGGCCACTCTCTGCTCACTGGGGCTCTATGAGGCCAT  
55 TACTGTGTGCTGTGATGCACATATCTTCGGCTGCTGGACGCTATAAGGCTTTTCCACCTGT  
GCCTCTCATCTCACTGTGTGTGATAATCTTCTATGACGCCAGTATCTTCACTATATGCTGGCC

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTACTGTATGCTGTCATTGTGA  
CCATTGCTCAATCCCATCATTTACTGCTGCGCAATCAAGAGGTCAAGAGAGCCCTATGCT  
GTACTCTGCCACCTGTACCGACCAAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA  
G (SEQ ID NO: 424).

5

**AOLFR227 sequences:**

MEPQNTSTVTNQLLGFQNLLEWQALLFVIFLLIYCLTHGNVVIITVVSQGLRLHSPMYMFLQH  
LSFEVWVYSTTVPLLLANLLSWGQAIJSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP  
LRYEPLMHRRGLCARLVVSVWCTGTVSTGFLHSMMSIRLDFCGRNQINHFCDLPPLMQLSCSR  
YITEVTILHLSIAVLICIFFLTLGPYVIVVSSILRIPSTSGRRKTFSTCGSHLAVVTLYYGTMISMYV  
CPSPHLLPEINKHISVFYTVVTPLLNPVIYSLRNKDFKEAVRKVMRRKCGILWTSKRKF  
LY (SEQ ID NO: 425).

ATGGAGCCCCAAAATACCTCCACTGTGACTAACTTTCAGCTGTAGGATTCCAGAACCTTC  
15 TTGAATGGCAGGCCCTGCTCTTGTGATTTTCTGCTGCTACTACTGCCTGACCATATAGGGA  
AATGTTGTGATCATACACCGTGGTGAGCCAGGCCCTGCGACTGCACTCCCTATGTACATGT  
TCTCTCAGCATCTCTCTCTTCTGGAGGTCTGGTACACGTCACACCTGCTGCGCCCTCTCTCTA  
GCCAACCTGCTGCTCTGGGCCCAAGCATCTCTCTCTGCTGCATGGCAGCACTCATCT  
TCTTCGTATTCTCTCGGCCACCGAGTGCTTCTCTGCGGCTTCATGGCCTATGACCGTTAC  
20 CTGGCCATCTGCAGCCCATCCGCTACCCCTTCTCATGCATCGTGGGCTATGTGCCAGGTT  
GGTGGTGGTCTCATGTGTGACAGGGGTGACGACAGGCTTCTGCTATCCATGTGATGATTTC  
AGGTTGGACTTCTGTGGGCGCAATCAGATTAACCATTTCTCTGCGACCTCCCGCCACTCA  
TGCAGCTCTCTGTTCCAGAGTTTATATCACCGAGGTGACCATCTTCATCTGTCAATGGC  
GTGCTGTGCACTTGTCTTTTCTGACACTGGGCGCCTATGTTTTCATGTGTCTCCATATT  
25 GAGAACTCTCCACCTCTGGCCGGAGAAGACCTTTCCACATGTGGCTCCACCTGGCT  
GTGTCACTCTCTACTAGGGACCATGATCTCCATGTATGTGTGCCAGTCCCACTGGT  
GCCTGAAATCAACAAGATCATTTCTGTCTTCTACACTGTGGTGACACCACTGCTGAACCA  
GATTATCAGCTTGAGGAACAAAGACTTCAAAGAAGCTGTGAAGAAGGTATGAGAAGG  
AAATGTGGTATTCTATGGAGTACAAGTAAAGGAAGTTCTTTATTAG (SEQ ID NO: 426).

30

**AOLFR229 sequences:**

MFYVNQIPQLYHISFVYPTELWSRAIIPCMPTLSFWVCSATPVSPGFFALILLVFTSIASNVVK  
IILIHIDSRHLTPMYFLLSQLSLRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYTLAGEA  
FLLGLMSCDRYVAICNPLHPYDLMRSRKICWLIVAAA WLGGSIDGFLLPVTVMQFPFCASREIN  
35 HFFCEVPALLKLSCTDSAYETAMYVCCIMMLLIPFSVISGSYTRILITYVRMSEAEGRKAVAT  
CSEHVMVYSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTLTPMLNPLIYSLRNKYDTGALQK  
VVGRCVSSGKVYTF (SEQ ID NO: 427).

ATGTTTATGTAAATCAGATACCTTTCCAACCTTATCATATCTCTTTCTGTGACCTACAGA  
40 GCTATGGAGCAGAGCAATTATTCGCTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCA  
ACGCCGTTTCCCGTGGCTTCTTTGCCCTCATCTCTCGGCTTGTGTGACCTCCATAGCCAG  
CAACGTGGTCAAGATCATCTCATCCACATAGACTCCCGCTCCACACGCCCATGTACTTC  
CTGCTAGCCAGCATCTCCCTCAGGGACATCCTGTATATTTCCACCATGTGGCCAAAATGCT  
GGTCAGCCAGGTGATGAGCCAGAGAGCCATTTCTTTGCTGGATGCATGCCCCAACACTTC  
45 CTCTACTGACCTTAGCAGGGGCTGAGTTCTCTCTCCTAGGACATGATGCTGTGATCGCTA  
CGTAGCCATCTGCAACCTCTGCACTATCTGACCTCATGAGCCGCAAGATCTGCTGGTTG  
ATTGTGGCGCGCAGCTGGCTGGGAGGGTCTATCGATGGTTTCTTGTGCACTCCCGCTCAGCA  
TGCAGTTCCTCTTCTGTGCTCTCGGGAGATCAACCACTTCTTCTGCGAGGCTGCTGCCCTT  
CTGAAGCTCTCTGCAACGGACATCAGCCTACGAGACAGCATGTATGTCTGCTGATTAT  
50 TGATGCTCTCATCTCTTCTCTGTGATCTCGGGCTCTTACACAAAGATTTCTATTACTGTT  
TATAGGATGAGCGAGGAGAGGGGAGGCGAAAGGCTGTGGCCACTGCTCTCACACATGT  
GTGGTTGTGACGCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCTCATCTTACCA  
CACCCCTGAGCAGGACAAAGCTGTATCTGCTTTTACACCATCTCTACTCCATGCTCAAT  
55 CCACTCATTTACAGCTTAGGAACAAGGATGTCACGGGGCCCTACAGAAGGTTGTTGGG  
AGGTGTGTGCTCTCAGGAAGTAACCACTTTCTAA (SEQ ID NO: 428).

**AOLFR230 sequences:**

MGMEGLLQNSTNFTVLGTIHPAFPGLLFAIVFSIFVVAITANLVMILLIHMSRLHTPMYFLLS  
 QLSIMDTIYICITVPKMLQDILLSKDKTISFLGCAVQIFLYLTLLGGEFFLLGLMAYDRYVAVCNP  
 LRYPLLMNRRVCLFMVVGWSVGGSLDGFMLTPVMTSFPFCSRSEINHFFCEIPAVLKLSCTDTS  
 5 LYETLMYACCVLMMLPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVSVFYGAIFY  
 TNVLPHSYHTPEKDKVVSAFYTILPMLNPLIYSLRNKDVAALRKVLGRGSSQSIRVATVIR  
 KG (SEQ ID NO: 429).

ATGGGCATGGAGGGGTCTTCTCCAGAACTCCAATACTTCGTCTCCACAGGCTCATCACCC  
 10 ATCCTGCCITCCCCGGGCTTCTCTTTGCAATAGTCTTCTCCATCTTTGTGGTGGCTATAACA  
 GCGCAACTTGGTCAATGATTTCTGCTCATCCACATGGACTCCCGCTCCACACACCATGTGACTT  
 CTTGTCTCAGCCAGCTCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCCAAGATGC  
 TCCAGGACCTCCTGTCCAAAGGACAAGACCAATTCTCTCTGGGGCTGTGCAGTTACAGATCTT  
 CCTCTACCTGACCCTGATTGGAGGGGAATTCTCTCTGCTGGGTCTCATGGCCTATGACCGC  
 15 TATGTGGCTGTGTGCAACCTCTACGGTACCTCTCCTCATGAACCGCAGGTTTGCTTATT  
 CATGGTGGTGGGTCTCTGGGTGGTGGTCTCTGGATGGGTTCATGCTGACTCTGTCACT  
 ATGAGTTTCCCCTCTGTAGATCCCGAGAGATCAATCACTTTTCTGTGAGATCCGAGCCGT  
 GCTGAAGTTGTCTGTGCACAGACACGTCACTCTATGAGACCCGTGATGTA TGCTGTCTGCGTG  
 CTGATGCTGCTTATCCCTCTATCTGTATCTCTGTCTCTACACGCACATCTCTCTGACTGT  
 20 CCACAGGATGAACCTCTGTGTGAGGGCGCGCGCAAAAGCTTTGCTACGTGTTCTCTCCACATT  
 ATGGTGGTGTGAGCGTTTCTACGGGGCAGCGCTTCTACACCAACGTGCTGCCCCACTCTTACC  
 ACACCTCCAGAGAAAGATAAAGTGGTGTCTGCTCTTACACCATCTCTACCCCATGCTCAA  
 CCCACTCATCTACAGCTTGAGGAATAAGATGTGGCTGCGAGCTCTGAGGAAAGTACTAGG  
 GAGATGTGGTCTCTCCAGAGCATCAGGTTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID  
 25 NO: 430).

**AOLFR231 sequences:**

MERANHSVSEFILLGLSKSQNLQILFGLFVSFVFGIVLGNLLILVTVFDSLHTPMYFLLSNL  
 SCDIMILASFAITPKMIVDFLRERKTISWGCYSQMFHMLLGGSEMMLLVAMAIKDRYVAICKP  
 30 LHYMTIMSPRVLTGLSSYAVGVHSSQMAFMLTLPFCGPNVDSFFCDLPVILKACKDITYI  
 LQLLVADSGLLSLVCFLLLVSYGVHFSVRYRAASRSSKAFSTLSAHTVTVTLFAPCVFIYVW  
 PFSRYSDVKILSVFYTIPTPLNPIHYTLRNQEVKAIAKKRLCI (SEQ ID NO: 431).

ATGGAAGAGCAAACCATTCAGTGGTATCGGAATTTATTTGTGGGACTTTCACCAATCTC  
 35 AAAATCTCAGATTTTATTCTCTTGGGATCTCTGTGGTCTCTGTGGGATGTGTAGGA  
 AACCTGCTCATCTTGGTGACTGTGACCTTTGATTCGTCTCTCACACCAATGTATTTTCT  
 GCTTAGCAACCTCTCTCTGATGATATGATCTCTGGCTCTTTTGTACCCCTAAGATGATTG  
 TAGATTTCTCTCGAGAACGTAAGACCATCTCATGGTGGGATGTTATTCAGAGATGTTCTT  
 40 TATGCACTCTCTGGGTGGGAGTGAGATGATGTTGCTTGTAGCCATGGCAATAGACAGGAT  
 GTTGCCATATGCAAAACCCCTCCAATTACATGACCATCATGAGCCACGGGTGCTCACTGGGC  
 TACTGTTATCTCTCTATGCACTTGGATTGTGCACTCATCTAGTCAAATGGCTTTCATGTG  
 ACTTTGCCCTCTCTGGTCCCAATGTTATAGACAGCTTTTCTGTGACCTTCCCCTGTGAT  
 TAAACTTGCTCTGCAAGGACACCTACATCTACAGCTCTGTGTCATTGCTGACAGTGGGCTC  
 45 CTGCTCACTGGTCTGCTTCTCTCTTGTCTGTCTCTATGAGAGTCAATAATTCTCAGTTG  
 GTACCGTGTGCTAGTGCGATCTCTTAAGGCTTTCTCCACTCTCTGACTACATACAGTGT  
 TGACTCTGTTCTTGTGCTCGGTGTGCTTTATCTACGTCTGGCCCTTCAAGCATCTGGGTA  
 GATAAAATCTTCTGTGTTTACACAAATTTACACACTCTCTAAATCTCTATTATTATAC  
 ATTAAGAAATCAAGAGGTAAAGCAGCCATTAAAAAAGACTCTGCATATAA (SEQ ID NO:  
 432).

**AOLFR232 sequences:**

MDNITWMASHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV  
 VIFVFLMALSGNAVILLIHCDLHHTPMYFFISQLSLMDMAYISVTPVKMLLDQVMGVNKS  
 APEGCGMFFYVTLAGEFFLLATMAYDRYVAICHPRLYFVLMNHRVCLFLSSGCWFLGSDV  
 55 GFTTFPTMTPTFPRGSRHEHFFCEVPAVLNLSCSDTSLYEIFMYLCVLMILPVYIISVLLILL

TIHGMNSAEGRKKAFATCSSHLTVVILFYGAAIYTYMLPSSYHTPEKDDMMVSVFYTLTPVVPN  
LIYSLRKNKDVGMALKKMLTVEPAFQKAME (SEQ ID NO: 433).

5 ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTGGGATTTCATCTCTGATGGGAC  
TCTTCAGACAATCCAAACATCCAAATGGCCAATATCACCTGGATGGCCAACCAACACCTGGATG  
GTCGGGATTTTCATCTCTGTGGGACTCTTCAGACAATCCAAACATCCAGCACTACTTTGTGTG  
GTCATTTTGTGGTGTCTCTGATGGCGTGTCTGGAAATGCTGTCTGTCTCTGTATACATACA  
TGCGAGCCCACTCCACACCCCATGTACTTTTCATCAGTCAATTGTCTCTCATGGAGCA  
TGGCGTACATTTCTGTCACTGTGCCAAGATGCTCCTGGACCAGGTATGGGTGTGAATAA  
10 TGCTGACCCCTTGAGTGTGGGATGCAGATGTTCTTACGTGACACTGACAGTTCAGAA  
TTTTCTCTAGCCACCATGGCCTATGACCGCTACGTGGCCATCTGCCATCTCTCCGTTA  
CCCTGTCTCATGAACCATAGGGTGTGTCTCTCTGTATCAGGCTGCTGGTTCCTGGGCT  
CAGTGGATGGCTTCAATTCACCTCCCATCACCATGACCTTCCCTTCCGTGGATCCCGGGA  
GATTATCATTTCTCTGTGAAGTTCCTGTGTATTGAATCTCTCTGCTCAGACACCTCAC  
15 TCTATGAGATTTTCATGTACTTGTGCTGTGCTCATGCTCCTCATCCCTGTGGTGTATCATT  
TCAAGTCTCTATTACTCATCTCTCTCACCATCCACGGGATGAATCAGCAGAGGGGCGGA  
AAAAGGCTTTGGCCACTGCTCTCCCACTGACTGTGTCATCTCTCTATGGGGCTGCC  
ATCTACACCTACATGCTCCCACTCTCAACACCCCTGAGAAGGACATGATGGTATCTG  
TCTTCTATACCATCTCTCACTCCAGTGGTGAACCTTTAATCTATAGTCTTAGGAATAAGGAT  
20 GTCATGGGGCTCTGAAGAAAATGTTAACAGTGGAACCTGCCTTTCAAAAAGCTATGGAG  
TAG (SEQ ID NO: 434).

**AOLFR233 sequences:**

25 MANITRMANHTGKGLDFILMGLFRRSKHPALLSVIFVFLKALSGNAVILLIHCDAHLHSPMY  
FFISQLSLMDMAYISVTPVKMLLDQVMGVNKVSAPECGMQMFLYLTLAGSEFLTATMAYDR  
YVAICHPRLPYPLMNHVRCLFLASGCVFLGSVDGFMLTPTTMSFFCRSWEIHFFCEVPVITI  
LSCSDTYLTYETLMLCCVLMILLIPVTIISYLLILLTVHRMNSAEGRKKAFATCSSHLTVVILFY  
GAADYTYMLPSSYHTPEKDDMMVSVFYTLTPVNLPIYSLRKNKDVGMALKKMLTVRFRVL  
(SEQ ID NO: 435).  
30  
ATGGCCAACATCACCAAGGATGGCCAACCACTGGAAAGTTGGATTTCATCTCATGGGAC  
TCTTCAGACGATCCAAACATCCAGCTCTACTTAGTGTGGTCACTTTGTGGTTTTCTGTAAG  
GCGTTGTCTGGAATGCTGTCTGTATCCTTCTGATACACTGTGACGCCACCTCCACAGCC  
CCATGTACTTTTCATCAGTCAATTGTCTCTCATGGACATGGCGTACATTTCTGTCACTGTG  
35 CCAAGATGCTCCTGGACCAGGTATGGGTGTGAATAAGGTCTCAGCCCTGAGTGTGGG  
ATGCAGATGTCTCTATCTGACACTAGCAGGTTCTGGAATTTTCTCTTAGCCACCATGGC  
CTATGACCGCTACGTGGCCATCTGCCATCTCTCCGTTACCTGTCTCATGAACCATAGG  
GTCTGTCTTTTCTGGCATCGGGCTGTGTTCTCTGGGCTCAGTGAATGGCTTCATGCTCAC  
TCCCATCACCATGAGGCTTCCCTTCTGCAGATCTCTGGGAGATTATCATCTTTCTCTGTAAG  
40 TCCCTGCTGTAAAGCATCTGCTGTCTGCTCAGACACCTCACTATGAGACCTTCATGACTTA  
TGCTGTGCTCATGTCTCTCATCCTGTGACGATCATTTCAAGCTCCTATTACTCATCTCT  
CCTACCGTCCACAGGATGAATCAGCAGAGGGCGGAAAGGCTTTGGCCACTGTCTC  
CTCCCACTGACTGTGGTGTATCTCTTCTATGGGGCTGGCGCTCATACCTACATGCTCCCCA  
GCTCTACCAACACCTCTGAGAAGGACATGATGGTATCTGTCTTCTATACCATCTCACTCC  
45 GGTGCTGAACCTTTAATCTATAGTCTTAGGAATAAGGATGTCTATGGGGCTCTGAAGAAA  
ATGTTAACTGTGAGATTCTCTTTAG (SEQ ID NO: 436).

**AOLFR234 sequences:**

50 MPNSTTVMEFLMRFSVDVTLQILHSASFFMLYVLTLMGNLIVTVTTCDSSLHMPMYFFLRN  
LGLTDACYISVTPYTSVNSLLDSTISKAGCVAQVFLVVFVYVELLFTIMAHDRYVAVCQPL  
HYPVIVNSRICQMTLASLLSLVYAGMHTGSTFQLPFCRSNVIHQFFCDIPSLKLSCTSDTFSNE  
VMIVVSALGVGGGCFIIRSYIHIFSTVLGPPRGADRTKAFSTCIPHILVSVFLSSCSSVYLRFP  
AIPAAATQDLILSGFYSIMPLFNPIIYSLRKNQKVAIKKIMKRIFYSENV (SEQ ID NO: 437).  
55 ATGCCCAATTCAACCACCGTATGGAATTTCTCTCATGAGGTTTCTGTATGTGTGGACAC  
TACAGATTTTACATTCTGCATCTTCTTATGTGTATTGGTAACTCTAATGGGAAACATC

CTCATTGTGACCGTGACACCTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCTCAG  
 GAATCTGTCTATCTTGGATGCCTGCTACATTTCTGTTACAGTCCCTACCTCATGTGTCAATT  
 CCCTACTGGACAGCACCACCATTTCTAAGCGGGATGTGTAGCTCAGGCTCTCTCGTGGT  
 TTTTTTTGTATATGTGGAGCTTCTGTTTCTACCATTTATGGCTCATGACCGCTATGTGGCTG  
 5 TCTGCCAGCCACTTCACTACCTGTGATCGTGAACCTCGAATCTGCATCCAGATGACACT  
 GGCCTCCCTACTCAGTGGTCTTGTCTATGCAGGCATGCACACTGGCAGCACAATCCAGCTG  
 CCCTTCTGTCGGTCCAACGTTATTCATCAATTTCTGTGACATCCCTCTCTCTGATGAAGCT  
 CTCTTGCTCTGACACCTTCAGCAATGAGGTCATGATTGTGTCTCTGCTCTGGGGTAGGT  
 TGGCGCTGTTTCACTTTATCATCAGGCTTACATTCACATCTTTTCGACCGTGTCTGGGTT  
 10 TCCAAAGGAGGACAGACAACAAAGGCTTTTCCACCTGCATCCCTCATCATCTCTGGTGGT  
 TCAGTCTTCTCAGTTCATGCTCTTCTGTGTACTCAGGCCACTGCGATACCTGCAGCCAC  
 CCAGGATCTGATCCTTCTGTTTATTCCATAATGCCTCCCTCTTTAACTGATTTTATA  
 CAGTCTTAGAAATAAGCAATAAAGGTGGCCATCAAGAAAATCATGAAGAGAATTTTTTA  
 TTCAGAAAAATGTGTAA (SEQ ID NO: 438).

**AOLFR235 sequences:**  
 MDGYNSSLQGFVLMGISDHPQLEMIFFIAILFSYLLTLLGNSTIILSRLEARLHTPMYFFLSNL  
 SSLDLAFATSSVPMQLINLWPGKTSISYGGCTQLYVFLWLGAATECILLVMAFDRIYAVRCPL  
 RYTAIMNPQLCWLLAVIACLGGGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL  
 20 NQAVLNGVCTFFTAVPLSIHIVSYCLIAQAVLKIRSAEGRRKAFNTCLSHLLVFLFYGSAYGY  
 LLPAKNSKQDQKKFISLFYSLVTPMVNPLIYTLRNMVEVKALRRLGLKGREVG (SEQ ID NO:  
 439).

ATGGACGGGGTGAATGATAGCTCCTTGCAGGGCTTGTCTGTATGGGCATATCAGACCATC  
 25 CCGAGCTGGAGATGACTTTTTATAGCCATCCTCTTCTCTCTATTTGCTGACCCCTACTGGG  
 AACTCAACCATCATCTTGCTTTCCGGCTGGAGGCCGGCTCCATACACCCATGTACTTCTT  
 CCTCAGCAACCTCTCTCCTTGGACCTTGTCTTTCGTACTAGTTCAGTCCCAATGCTGA  
 TCAATTTATGGGGACCAAGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTCTATGT  
 CTTCCTTTGGCTGGGGGCCACCGAGTGATCCTGCTGGTGGTGTGGCATTTGACCGCTAC  
 30 GTGGCAGTGTGCGCGCCCTCCGCTACACCGCCATCATGAACCCCAAGCTCTGCTGGCTGT  
 TGGCTGTGATTGCTGCCTGGGTGGCTGGGCAACTCTGTGATCCAGTCAACATCTCACTCT  
 GCACTGCCATTGTGTGGGCACCGGAGGGTGGAGGGATTCTCTCGAGAGTCTGCTGCCAT  
 GATCAAACTGGCTGTGGGCACACAAGTCTCAACACAGGCTGTGCTCAATGGTGTCTGCACC  
 TTCTTCACTGCAAGTCCCACTAAGCATCATCGTGATCTCCTACTGCTCATTGCTCAGGAGT  
 35 GCTGAAAATCCGCTCTGCAGAGGGGAGGGCAAGGCGTTCAATACGTGCTCTCCCATCT  
 GCTGGTGAGTTCCTCTTCTATGGCTCAGCCAGCTATGGGATCTGCTTCCGGCCAAGAAC  
 ACCTCAAGGACAGGCAAGGTTCATTTCCCTGTTCTACTCGTGTGTCACACCCATCGGTGA  
 ATCCCTCATCTACAGCTGCGGAACATGGAAGTGAAGGGCGCACTGAGGAGGTGTGCTGG  
 GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

**AOLFR236 sequences:**  
 MTSQERDIAYSINVSFAKGMTSRSVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLLFL  
 LFLLYSITVAGNLLILLTVGSDSHLSLPMYHFLGHSFLDACLSTVTVPKVMAGLLTLDGKVIS  
 FEBCAVOLYCFHFLASTECFLYTVMAVDRYLAICQPLHYPVAMNRRMCMAEMAGTWAIGATH  
 45 AAHIHLSLIFRLLYCGPCHIAFYFCDIPPVKLACTDITINELVMLASIGIVAAGCLLIVISYIFVA  
 AVLRIQTAQGRQRAFSPCTAQLTGVLVLYVPPVCYILQPRSEAGAGAPAVFYITVPMNLNPFY  
 TLRNKEVKKHALQKSSFFRESTAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTTATCCATTAAATGTCAGTTTGTGTGCAAAAGG  
 50 GGATGACTAGCCGCTCTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACGAGA  
 CTGTGGTGAGCCACTTCTTCTGGAGGGTTTGAAGGTACACCGCTAAACATTTAGCCGCTCT  
 TTCTCTCTCTTCTCTCTCATCTACAGCATCACTGTGGCTGGGAATCTCTCATCTCTCTAA  
 CTGTGGGCTCTGACTCTACCTCAGCTTACCCATGTACCACTTCTCTGGGGCACTCTCTTCT  
 CTGGATGCTCTGTGTGTACAGTGACAGTGCCCAAGGTCATGGCAGGCTGCTGACTCTGG  
 55 ATGGGAAGGTGATCTCTTGTAGGGCTGTGCGGTACAGCTTATGTGCTTCCATTTCTGGC  
 CAGCATGAGTGCTTCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAAA

CCCTGCACTACCCAGTGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC  
TGGGCCATAGGTGCCACGCACGCTGCAATCCACACCTCCCTACCTTCCCGCTGCTCTACT  
GTGGGCTTGGCCATATGGCTACTTCTTCTGCGACATACCCCTGTCTCTAAAGCTGGCTGT  
ACAGACACCACCATTAATGAGCTAGTCATGCTTGGCAGCATTTGGCATCGTGGGTGACAGGCT  
5 GCTCATCTCTCATCTGTATTTCCTACATCTTCATCGTGGCAGCTGTGTTGGCGCATCCGCACA  
GCCACGGGCGGACGCGGGCTTCTCCCTGCACTGCCAGCTCAGTGGGGTGCCTCTGT  
ACTACGTGCCACCTGTCTGTATCTACCTGCAAGCTCGCTCCAGTGAGGCGAGGAGCTGGGC  
CCCTGCTGTCTTACACAATCGTAACCTCAAAGCTCAACCATTCATTACACTTTGCGGA  
10 ACAAGGAGGTGAAGCATGCTCTGCAAGGCTTTTGTGCAGCAGCTTCCGAGAGTCTACAG  
CAGGCAGCCACCCCATAG (SEQ ID NO: 442).

#### AOLFR237 sequences:

MDQRNYTRVKEFTFLGITQSRELSQVLFVFLVYMTLMGNFLIMVTVTCESHLTPMYFLL  
RNLSDICFSSITAPKVLIDLLSEKTSISFGCVTQMFFHLLGGADVFSLVMAFDRIYIAISKPL  
15 HYMTIMSRGRCTGLIVGFLGGGLVHSIAQISLLPLPVCGPVNLDTFYCDVPQVLKACTDFT  
LELLMISNGLVSWVFVFFLLISYTVILMMLRSHITGEGRRKAISTCTSHITVTVLHFVPCIVYA  
RPFALTPTDAISVTFVISPLNPIHYTLRNQEMKLAMRKLKRLGQSERLIQ (SEQ ID NO:  
443).

20 ATGGATCAGAGAAATTACACCAGAGTGAAAGAAATTTACCTTCTGGGAATTACTCAGTCCC  
GAGAACTGAGCCAGGTCTTATTTACCTTCTGTTTTGGGTGATCATGACAACCTAATGGG  
AAACTTCTCATCATGGTTACAGTTACCTGTGAATCTCACCTTCATACGCCCATGTACTTCC  
TGCTCCGCAACCTGCTATTTCTTGACATCTGCTTTTCTCCATACAGCTCTCAAGGCTCGT  
ATAGACTCTTATCAGAGACAAAACCATCTCCTTCAGTGGCTGTGTCACCTAAATGTTCT  
25 TCTTCCACCTTCTGGGGGAGCAGACGCTTTTCTCTCTCTGTGATGGCGTTTGACCGCTAT  
ATAGCCATCTCCAAGCCCCGTCACATATGACCATCATGAGTAGGGGGCGATGACAGGGC  
TCATCTGGGCTCTCTGGGTGGGGGGCTGTGCCACTCCATAGCGCAGATTTCTCTATTGCT  
CCCCTCCCTGTCTGTGGACCAATGTCTTGACACTTCTACTGCGATGTCCCCAGGTCC  
TCAAACTTGCTGCTGACGACACTTCACTCTGGAGCTCCTGATGATTCAAAATGATGGGTT  
30 AGTCAGTGTGTTGTAATTTCTTCTTCTTCTCATATCTACACGGTCACTTGATGATGTGA  
GGTCTCACCTGGGGAAGGAGGAGGAAAGCCATCTCCACCTGCACCTCCACATACCCG  
TGGTGACCTGCAATTTCTGTGCCCTGCATCTATGCTATGCCCCGGCCCTTCACTGCCCTCCC  
ACAGACATGCAATCTCTGTCACTTCACTGTCTCTCCCTTGTCTCAATCTATAATTTA  
CACGCTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAACTGAAGAGACGGCTAGGAC  
35 AATCAGAAAGGATTTAATCAATAA (SEQ ID NO: 444).

#### AOLFR238 sequences:

MAPENFTRVTEFILTGVSSCPQLQPLFLVFLVLYVTMAGNLGHTLTSVDSRLQTPMYFFLRHL  
AINDLONSTVIAPKMLMNFVKKKTSFYECATQLGGFLFFVSEVMMLAVMAYDRYVAICNP  
40 LLVMVVSRLCLLLVSLTYLYGFSTAIVVSPCIFSVSYCSSNINHFYCDIAPLLALSCSDTYIPE  
TIVFISAATNLFFSMITVLVSYFNIVLSILRIRSEPRKKAFSTCASHMIAVTVFYGTMLFMYLQ  
QTNHSLDIDKMASVFYTLVIPMLNPLYSLRNDNVNVALKFMENPCYSFKSM (SEQ ID NO:  
445).

45 ATGGCTCTGAAAATTTACACAGGCTACTGAGTTTATTTCTACAGGTGTCTTAGCTGTC  
CAGAGCTCAGATTCCCTCTTCTGGTCTTCTAGTGCTCTATGTGCTGACCATGGCAGG  
GAACCTGGGCATCATACCCCTACCAAGTGTGACTTCGACTTCAAACCCCCATGATTTT  
TCTTGAGACATCTAGCTATCATCAATCTTGGAACCTCTACTGTCAATTGCCCTTAAATGCTG  
ATGAACCTTTTAGTAAAGAGAAACTACCTCATCTATGAATGTGCCACCAACCTGGGAG  
50 GGTCTGTGTTCTTATGTATCGGAGGTAATGATGCTGGCTGTGATGGCTATGACCGCTA  
TGTGGCCATTTGTAACCCCTGCTCTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCTGCT  
TGGTGGCTCTGCTGACTCTATGGCTTTTACAGCTAATGTGGTTTACCTTGTATATTCT  
TCTGTGCTTATTTGCTCTTCTAATATAATCAATATTTTACTGTGATATTGCACTTCTGT  
AGCATTATCTTGCTCTGATACTACATACACAGAAACAATAGTCTTTATATCTGCAGCAACA  
55 AATTGTTTTTTCATGATTACAGTTCTAGTATCTTATTTCAATATTGTTTGTCCATTCTA  
AGGATACGTTACACAGAAGGAAGGAAAAAGCCTTTTCCACCTGCGCTTCGATATGATA

GCAGTCAACGGTTTCTATGTTGGGACAATGCTATTTATGTATTGTCAGCCCCAAACCAACCACT  
CACTGGATACTGATAAGATGGCTTCTGTGTTTACACATTGGTGATTCTCATGTGTAATCC  
CTTGATCTACAGCCTGAGGAATAATGATGTAATGTTCCCTTAAAGAAATTCATGGAATAA  
CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

5

**AOLFR239 sequences:**

MDPQNSYSLVSEFVLHGLCTSRHLQNFFIFFGGVYVAIMLGNLLILVTVISDPCLHSSPMYFLLG  
NLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMQIFLHFTGGAEMVLLVSMAYDRYVAIC  
KPLHYMTLMSWQTCIRLVLASVWVGVHHSISQVAFVNLPHYCGPNEVDSFFCDLPLVIKLACM  
10 DTYVLIHIMISDSGLLSCLFLLLSYTVILLAIRQAAGSTSKALSCTSAHIMVVLITFFGPCIIF  
YVPPSRFSVDKLLSVFYTFITPLLNPIYTLRNEEMKAMKKLQNRRTVFQ (SEQ ID NO: 447).

15

ATGGACCCACAGAACTATTCCTTGGTGTACAGAAATTTGTGTGCTAGGACTGTGCACITTCAC  
GACATCTCAAAAATTTTTCTTTATATTTTTCTTTGGGGTCTATGTGGCCATTATGCTGGGT  
AACTCTTCAATTTTGGTCACTGTAATTTCTGATCCCTGCCTGCACCTCCTCCCTATGTACTT  
CCTGTGGGGGAACCTAGCTTTCTGGACATGTGGCTGGCCCTCATTTGCCACTCCCAAGATG  
ATCAGGGATTTCTTATGTATCAAAAACCTCATCTCCTTTGGAGGATGATGTGGCTCAAACT  
TCTTTCTGCACATTCTGTGGGGCTGAGATGGTGTCTCGTTTCCATGGCCATGACAG  
ATATGTGGCCATGCAAAACCTTGCAATACATGACTTTGATGAGTTGGCAGACTTGCATC  
20 AGGCTGGTGTCTGGCTTCATGGGTCTGTGGATTTGTGCACTCCATCAGCTAAGTGGCTTCA  
CTGTAAATTTGCTTACTGTGGCCCCAATGAGGTAGACAGCTTCTTCTGTGACCTCCCTCTG  
GTGATCAAACTTGCCCTGCATGTGACACCTATGTCTTGGGATAAATATGATCTCAGACAGTG  
GGTTGCTTTCTCTTGAAGTGTCTTCTGCTCCTCTGATCTCCTACACCGTGATCCTCTCGCT  
ATCAGACAGCGTGTCTGCCGTAGCACATCAAAGCACTCTCCACTTGCTCTGCACATATCA  
25 TGGTAGTGACGCTGTCTTTGGCCCTTGCAATTTTGTGTTATGTGCGGCCCTTTCAGTAGGTTT  
TCTGTGGACAAGCTGTCTGTGTTTATAACCAATTTTATCTCCACTCCTGAACCCCAATTAT  
CTACACATTTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAACTGCAAAACCGACGGGT  
GACTTTTCAATGA (SEQ ID NO: 448).

30

**AOLFR240 sequences:**

MAGENHTTLPFLLGFSDLKALQGPLFWVVLLVYLVTLLGNSLIILLTQVSPALHSPMYFFLR  
QLSVVELFYTTDIVPRTLNLGSPHPQAIISFGCAAQMYFVILGISECCLLTAMAYDRYVAIC  
QPLRYSTLLSPRACLAMVGSSWLTGHTATTHASLIFSLPFRSHPIPHFLCDILPVLRLASAGKHR  
SEISVMTATTVFIMIPFLIVTSYRILGAILAMASTQSRRKVFSTCSSHLLVVSFFGTASITYRQP  
35 AGSSVTTDRVLSLFYTVITPMLNPIYTLRNKDVRRLRHLVKRQRPSP (SEQ ID NO: 449).

40

ATGGCTGGGGAAACCACTACACTGCCTGAATTCCTCCTTCTGGGATCTCTGACCTCA  
AGCCCTGACGGGCCCCCTGTTCTGGTGGTGTCTTCTGGTCTACCTGGTCACTTGTCTGGG  
TAACTCCCTGATCATCCCTCCTCACACAGGTGAGCCCTGCCCTGCACCTCCCCATGTACTTCT  
TCTGCGCCAACTCTCAGTGGTGGAGCTCTCTACCACTGACATCGTGCCAGGACCT  
GGCCAATCTGGGCTCCCCGCATCCCCAGGCCATCTCTTCCAGGGCTGTGCAGCCAGATG  
TAGCTCTGATTTGTCTGGGCATCTCGGAGTGTGCTGCTCACGGCCATGGCCCTATGACC  
GATATGTTGCCATCTGCCAGCCCTACGCTATTCCACCCTCTTGAGCCCAAGGGCTGCTT  
GGCCATGGTGGGGTCTCTGCTGCTCACAGGCATCATCACGGCCACCAACCCATGCTCTCCTC  
45 ATCTCTCTCTACCTTTTTCGACGCAACCCGATCATCCGCACTTTCTCTGTGACATCTGCG  
AGTACGTAGGCTGGCAAGTGTGGGAAGCACAGGAGCGAGATCTCCGTGATGACAGGCCAC  
CATAGTCTTCATTATGATCCCTTCTCTCTGATTGTCACTCTTACATCCGCATCTCTGGGTG  
CCATCTAGCAATGGCTCCACCCAGAGCCGCCGCAAGGTCTTCTCCACCTGCTCCTCCCA  
TCTGCTCTGTGGTCTCTCTCTCTTTTGGAAACAGCCAGCATCACTACCGGCCGAGGCA  
GGCTCTCTGTGTTACACAGACCGCGTCTCAGTCTCTTCTACACAGTACATCAACCCATGCT  
50 CAACCCCATCATCTACACCTTTCGGAACAAGGACGTGAGGAGGGCCCTGCGACACTTGGT  
GAAGAGGACGGGCCCTCACCCGA (SEQ ID NO: 450).

**AOLFR241 sequences:**

55

MPQLIFTYLYNMFYFFPLQLAENLTMVTEFLLGFSSSLGEIQLALFVVFLFLYLVLISGNVTIIS  
VIHLDKSLHTPMYFFLGILSTSETFYTFVILPKMLINLVSARTISFNCCALQMFFFLGFAITNCLL



LGVMGYDRIAACHPLHYPTLMSWQVCGKLAACAIGGFLASLTVNVNLFSLPFCSSANKVNH  
YFCDISAVILLACTNTDVFNEFVIFCGVLVLVVPFLFICVSVLILRTLKIPSAEGRKAFSTCAS  
HLSVVIHYGCASFIYLRPTANYVSNKDRLVTVTYTIVTPLLNPVMSLRNKDVLAIKRVLG  
KKGSLKLYN (SEQ ID NO: 451).

5

ATGCCCAAAATCTTATATTCACATACCTGAATATGTTTTACTTCTTCCCCCTTTGCAGAT  
CTTGGCAGAAAACCTCACCATTGGTCACCGAATCTCTGTGCTGGGTTTTTCCAGCCTTGGT  
GAAATTCAGCTGGCCCTCTTTGTAGTTTTTCTTTTCTGTATCTAGTCAATCTTAGTGGCAA  
TGTCACCAATATCAGTGTCTATCCACCTGGATAAAAGCCTCCACACACCAATGTACTTCTTC  
10 TTGGCAATCTCTCAACATCTGAGACCTTCTACACCTTGTCACTTCTACCCAAGATGCTCATC  
AATCTACTTCTGTGGCCAGGACAATCTCCTTCAACTGTTGTCTCTTCAAAATGTTCTTCTT  
CCTTGGTTTTGCCATTACCAACTGCCTGTCTATTGGGTGTGATGGGTTATGATCGCTATGCTG  
CCATTTGTGCACCTCTGCATTACCCCACTCTATGAGCTGGCAGGTTGTGCTGGAAAACCTGGC  
AGCTGCTGTGCAATTTGGTGGCTTCTTGGCCTCTCTTACAGTAGTAAATTTAGTTTTAGGCC  
15 TCCTTTTGTAGGCCCAACAAAGTCAATCAATCACTTCTGTGACATCTCAGCAGTCAATCTT  
TGCGCTTGTACCAACACAGATGTTAACGAAATTTGTGATATTCATTGTGGAGTCTTGTGAC  
TTGTGGTTCCCTTTCTGTTTATCTGTGTTCTTATCTCTGCAATCTGAGGACTATCCTGAAG  
ATTCCCTCAGCTGAGGGCAGACGGAAGCGTTTTCCACTGCGCCTCTCACTCAGTGTGTG  
TTATTTCTCAATTATGGCTGTGCTTCTCATCTACCTGAGGCCTACAGCAAACTATGTGTC  
20 ACAAAGACAGGCTGGTGACGGTGACATACACGAATGTGCACTCCTATCAACCCCACTG  
GTTTATAGCCTCAGAAACAAGGATGTCCAACCTGTCTACGAAAAGTGTGGGCAAGAAA  
GGTTCCTCTAAAACATATAAATTGA (SEQ ID NO: 452).

#### AOLFR242 sequences:

MNTTLFHPYSFLLGLIPGLESMLHWVGFFFAVFLTAVLGNITLFIQITDSSLHHPMFYFLAILS  
SIDPGLSTTIPKMLGTFWFTLREISFEGCLTQMFFHLCITGMESAVLVAMAYDCYVAICDPLCY  
25 TLVLTKNVSVSMALAFILRLPVFVPLFILRLPFQGHQIHPHTYGEHMGVHRYSCASIRVNIYIG  
LCAISILVFDIIAIVISYVQILCAVFLSSHDARLKAFTSCGSHVCVMLTFYMPAFFSMTHRFGR  
NIPHFHILLANFYVVIIPALNSVIYGVRTKQIRAVLKMFFNK (SEQ ID NO: 453).

30

ATGAATACCACTCTATTTTCATCTTACTCTTTCTTCTTCTGCGGAATCTCTGGGCTGGAAG  
ATGCACTCTCTGGGTTGGTTTTCTTTCTTTGCTGTGTTCTCTGACAGCTGTCTTGGGAATA  
TCACCATCTTTTGTGATTACAGACTGACAGTAGTCTCCATCATCCCATGTTCTACTCTG  
GCCATTCTGTCACTATTGACCCGGGCTGTCTACATCCACCATCCCTAAAAATGCTTGGCAC  
35 CTCTGTGTTACCTCTGAGAGAAATCTCCTTTGAAGGATGCCTTACCCAGATGTTCTCATCC  
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC  
CATCTGTGACCTTTTGTCTACAGTTGGTGTGCTGACAAACAAGGTGGTGCAGTTATGGCA  
CTGGCCATCTTTCTGAGACCTTATGCTTGTGTCATACCCCTTGTCTATTTATCTCAAGGCT  
TCCATTTTGTGGACACCAAAATATTCTCATACTTATGGTGAGCACATGGGCATTTGCCCGC  
40 CTGTCTGTGGCAGCATAGGGTTAAACATCATCTATGGCTTATGTGCCATCTCTATCTCTGGT  
CTTTGACATCATAGCAATTTGTCATTTCTATGTACAGATCCTTTGTGCTGTATTTCTACTCT  
TCTACATCATGACGACCTCAAGGCATTCAGCACCTGTGGCTCTCATGTGTGTGTCATGTT  
GACTTTCTATATGCTCTGCAITTTTCTCATTCATGACCCATAGGTTTGTGCGGAATATACCTC  
ACTTTATCCACACTCTTCTGGCTAAATTTCTATGTAGTCATTCACCTGCTCTCAACTCTGTA  
45 ATTTATGGTGTGCAACCAACAGATTAGAGCACAAAGTCTGAAAATGTTTTCAATAAAAT  
AA (SEQ ID NO: 454).

#### AOLFR243 sequences:

MEQVNKTVVREFVVLGFSSLARLQQLLFVILLLYLFTLGTNIIISTIVLDRALHTPMYFFLAIL  
SCSEICYTFVIVPKMLVDLLSQKKTISFLGCAIQMFSFLFGSSSHFLAAMGYDRYMAICNPLR  
50 YSVLMGGHGVCMGLMAAACAAGTFTSVLVTSLVFHLPFHSSNQLHHFFCDISPVKLKASHSRFG  
SQLVIFMLGVFALVIFLLLVIRIISAILKIPSSVGRYKTFSTCASHLVVTVHYSCASFIYLRPK  
TNYTSSQDTLISVSYTILTPLFNPVMSLRNKEFKSALRRITGQTFYPLS (SEQ ID NO: 455).

55

ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTGCTCCTCGGCTTCTCATCCTCGG  
CCAGGCTGCAGCAGCTGCTCTTGTATCTCTCTGCTCTACCTGTTCACTCTGGGCACC

AATGCAATCATCATTTCCACCAATTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT  
CCTTGCCATCCTTTCTTGCTCTGAGATTGCTATACCTTTGTCATTGTACCCAAGATGCTGG  
TTGACCTGCTGTGCCAAGAAGACCACTTTCTTCTGGGCTGTGCCATCCAAATGTTTTC  
TTCTCTTCTTTGGCTCTCTCACTCCTTCCTGCTGGCAGCCATGGGCTATGATCGCTATAT  
5 GGCCATCTGTAAACCCCACTGCGCTACTCAGTGCTCATGGGACATGGGGTGATGGGACTA  
ATGGCTCTGCTGCTGTGCTGTGGGTTCACTGTCTCCTGGTCACCACTCCCTAGTATTTC  
TCTGCGCTTCCACTCTCCAACCACTCCATCACTTCTCTGTGACATCTCCCTGTCCCTTA  
AACTGGCATCTCAGCACTCCGGCTTCAGTCAGCTGGTCATATTTCATGCTTGGTGTATTTC  
10 CTGGTCACTCTCTGCTACTTATCTAGTCTCCTACATCCGCATCATCTCTGCCATTCTAA  
AAATCCCTTCTCCGTTGGAAGATAACAAGACCTTCTCCACTGTGCTCTCCCTCATTTGTTG  
GTAACTGTTACACATACAGTTGTGCCTCTTTCATCTACTTAAGGCCCAAGACTAATTACACTTC  
AAGCCAAAGCTCCCTAATATCTGTGTATACCACTCTTACCCCATTTGTTCAATCCAAT  
ATTATAGTCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAACAATCGGCCAACT  
TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

15  
**AOLFR244 sequences:**

MWQEYVFLNVFFLLKVCCLTINSHVVILLPWECYHLIWKPLVIGTTVGSMEEYNTSSDTFT  
MGLFNRKETSGLIFAIISIFFTALMANGVMIFLIQTDRLHPTMYFLLSHLSDIMMYISTIVPKM  
LVNYLLDQRITISFVGCTAQHFLYLTLVGAEEFLLGLMAYDRYVAICNPLRYPVLMSSRRVCWMI  
20 IAGSWFGGLDGLLTPITMSFPFNSREINHFFCEAPVLKACADTALYETVMYVCCVLMML  
IPFSVVLASYARILLTVQCMSVVEGRKKAFATCSHMTVVSLSFYGAAMYTYMLPHSYHKPAQ  
DKVLSVFYITLTPMLNPLIYSLRNKDVGTGALKRALGRFKGQQRVSGGVF (SEQ ID NO: 457).

ATGTGGCAAGAATACTATTTTAAATGTTTCTTCCACTTTTAAAGTTTGTGCTGC2TAAC  
AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTGGAAGATAT  
CATCTTATATCGGCACACTGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT  
CACTTTTCATGGGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTITGGCAATCATCTCT  
ATCATCTTCTTACCGCACTGATGGCCAATGGGGTTATGATCTTCTGATCCAAACAGATT  
25 CTGGCCTCTATACACCATGTACTTCTCCTCAGCCACCTTCTCCTTAATTGACATGATGTAT  
ATTTCCACTAATTGCGCTTAAGATGCTGGTTAAITACCTGCTGGATCAAAGGACCATTTCTCT  
30 TGTGGGGTGACAGCTCAACACTTCTCTACCTTACCTTGTGGGAGCTGAAITCTTCTCTG  
CTGGGCTCATGGCCTATGACCGCTATGTGGCCTATTGCAACCTCTGAGATAACCTGTCT  
TCATGAGCGCCGGGTCTGTTGGATGATTATAGCAGGTTCTTGGTTTGGGGGCTCTTGGGA  
TGGCTTCTCTTAACCCCATCACCATGAGCTTTCCTTCTGCAATTCCCGGGAGATTAAACC  
35 ACTTCTTCTGTGAGGCACAGCAGTCTGGAAGTTGGCATGTGACAGACACAGCCCTCTACGA  
GCACAGTGAATGATGTGCTGTGTTTGTATGCTGCTGATTCCTTTCTGTAGTCTTGTCTT  
CCTATGCCGGAATCCTGACTACAGTTCACTGCTGATGAGCTCAGTGGAGGGCAGGAAGAAGG  
CATTTGCCACTTGTCTACCCACATGACTGTGGTGTCTTGTCTACGGGGCTGCCATGTAC  
ACCTACATGCTGCCACATCTTACCAACAGCCAGCCAGGACCAAGTCTCTCTGTGTTT  
40 ACACCATTTCTACACCATATGCTGAACCCCTCATCTACAGCCTTAGAAACAAGGATGTGAC  
TGGAGCTCTGAAGAGGGCCTTGGGAGGTTCAAGGGTCTCAAAGGGGTGTCAGGAGGTGT  
CTTTTGA (SEQ ID NO: 458).

**AOLFR245 sequences:**

MDLKNGSLVTEFILLGFFGRWELQIFFVFTSLIYGATVMGNILIMVTVTCRSTLHSPLYFLLGN  
LSFLDMCLSTATPKMIDLLTDHKTISVWGCVTQMFFMHFFGGAEMLTLIMAFDRYVAICKP  
LHYRTIMSHKLLKGFALISWIIFLHSIQIVLTMNLPFGCHNVNINIFCDLPLVIKLACIETYTLE  
LFVIADSGLLSFTCFILLVSYIVILVSPKSSHGLSKALSTLSAHIIIVTLFFGCPFIYVVPFSSL  
ASNKTILAVFTYVITPLNPSIYTLRNKKMQEAIKRLRFQYVSSAQNF (SEQ ID NO: 459).

ATGGATCTTAAAAATGGATCTCTAGTGACCGAGGTTATTTTACTAGGATTTTGGACGAT  
GGAACTTCAAAATCTTCTTCTTGTGACATTTCCCTGATCTACGGGTGATCTAGTGATGGGA  
AACATTCTCAATTATGGTCACAGTGACATGTAGGTCAACCCCTTCACTTCCCTGTACTTCT  
CCTTGGAAATCTCTCTTTTGGACATGTCTCTTCACTGGCACCAACCAAGATGATGA  
55 TAGATTGCTCACTGACCACAAGACCATCTCTGTGTGGGGCTGCGTGACCCAGATGTTCTT  
CATGCACTCTTTGGGGGTGCTGAGATGACTTCTTGATATCATGGCCTTTGACAGGAT

GTAGCCATATGTTAAACCCCTGCACATATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG  
TTTGCATATCTTTCATGGATAATTGGTTTTCACATCCATAAGCCAGATAGTTTAAACAAT  
GAACCTTGCCCTTCTGTGGCCACAATGTCATAAACACACATATTTTGTGATCTCCCTCTGTGA  
5 TCAAGCTTGCTTGCATTTGAAACATACACCCCTGGAATTAATTGTGATCTGCTGACAGGGGGCT  
GCTCTCTTTCACCTGTTTTCATCCTCTTGCTTGTTCATGTCATCTGCTGTCAGTGTACC  
AAAAAATCATCATATGGGCTCTCCAAGGCGCTGTCCACATTTGCTGCCACATCATTGTG  
GTCACTCTGTTCTTTGGACCTTGTAATTTTATCTATGTTGGCCATTCAGTAGTTTGGCAAG  
CAATAAACTCTTGGCGTATTTATACAGTTATCACACCCTTACTGAATCCGAGTATTATA  
10 CCTCGAGAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCCAATATGTTAGTT  
CTGCACAGAATTCTCTAG (SEQ ID NO: 460).

#### AOLFR246 sequences:

MSPENQSSVSEFLLGLPIRPEQQAVFTFLGMYLTTVLGNLLIMLLQLDLSHLTHPMYFFLSH  
LALTDISFSSVTPVKMLMDMRKYKSILYEICISQMYFFIFFDLDLSFLITSMAYDRYVAICHPI  
15 HYTVIMREELCVFLVAVSWILSCASSLSHLLTLRLSFCANHTPHVFCDLAALLKLCSDIFLNE  
LVMFTVGVVVITLPMFCILVSYGYGATILRVPSTKGHKLSTCGSHLSVVSLLYGYSGFYLF  
PLVSSSIDKDVIVALMYTVVTPMLNPFYLSLRNDRMKEALGKLFSTRATFFSW (SEQ ID NO:  
461).

20 ATGAGCCCTGAGAACACGAGCAGCGTGTCCGAGTTCTCTCTCTGGGCTCCCCATCCGGC  
CAGAGCAGCAGGCTGTGTCTTCAACCTGTCTCTGGGCATGTACCTGACCACGGTGTCTGGG  
GAACCTGTCTCATCTGCTGCTATCCAGCTGGACATCTCACCTTCACACCCCATGTACTTCT  
TCTCAGCCACTTGGCTCTCACTGACATCTCCTTTTCACTGTGCTGCTCCCTAAGATGCTG  
25 ATGGACATCGGGACTAAGTACAAATCGATCCTCTATGAGGAATGCAATTTCTCAGATGTATT  
TTTTTATAATTTTACTGACCTGGACAGCTTCTTATTACATCAATGGCATATGACCGATAT  
GTGGCATATGTACCCCTCTCCATACACTGTGTCATGATGAGGGAAGAGCTCTGTGTCTTCT  
AGTGGCTGTATCTTGGATCTGTGCTTTGTGCCAGCTCCCTCTCTCACACCCCTCTCCTGACCC  
GGCTGTCTTCTGTGCTGCGAACACCATCCCCCATGTCTTCTGTGACCTTGTCTGCCCTGCTC  
AAGCTGTCTCTGTCAGATATCTTCTCAATGAGCTGGTGTGTCACAGTAGGGGTGGTGG  
30 TCATTACCTGCCATCTGTGTATCCTGGTATCATATGGCATATGTGGGCCACCATCTGT  
AGGGTCCCTTCAACCAAGGGATCCACAAAGCATTTGTCCACATGTGGCTCCCATCTCTCTG  
TGGTGTCTCTAATTATGGGTCAATATTGGCCAGTACCTTTTCCGACTGTAAGCAGTTCT  
ATTGACAAAGGATGTCTATGTGGCTCTCATGTACACGGTGGTGCACACCCATGTGGAACCCCT  
TTATCTACGCCTTAGGAACAGGGACATGAAAGARGCCCTTGGGAACATCTTCAGTAGAG  
35 CAACATTTTCTCTTGTGTGATCTGACTTTTAAAAAATTAG (SEQ ID NO: 462).

#### AOLFR247 sequences:

MGQHNLTVLTEFILMELTRRPELQIPLGVFLVIYLTIVVGNLTMIILTKLDSHLTHPMYFSIRHL  
ASVDLGNSTVICPKVLANFVDRNTISYACAAQLAFLFMHIEFFILSAMAYDRYVAICNPILL  
40 YYVIMSQRQLCHVLVGQYLYSTFQALMFTIKIFLTFCGSNVISHFYCDVDPVLLPMLCSNAQEIL  
LLSILFSVFNLISSFLIVLSYMLILLAIQCMHSAEGRKKAFTSCGSHLTVVVVYFGSLLFMYMQ  
PNSTHFFDIDKMASVFYLLVPLMLNPLIYSLRNEEVKNAPYKLFEN (SEQ ID NO: 463).

ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCATTCTGATGGAACCTCACAAAGCGGC  
CTGAGCTGCAGATTCCTCTTTTGGAGTCTTCTCGTCACTACCTAATCACAGTGGTGGCG  
45 AACCTAACTATGATCAATTTGACCAAACTGGACTCCCACTTACATACACCATATGTACTTTC  
TATCAGACATTTGGCTTCTGTGTGATCTTGTAATCTTACTGTCAATTTGTCCCAAGGTGCTGG  
CAAAATTTTGTGTGGATCGAAATACTATTCTCTATTATGCATGTGCTGCACAGCTGGCATT  
TTCTTATGTTCATTATCAGTGAATTTTTCATCCTGTGACCATGGCCTATGACCGGTATGTG  
50 GGCCATTTGTAACTCCTCTGCTCTATTATGTATATATGTCTCAGCGACTGTGATGTGATGCT  
TGGGCATTCAAATATCTTACAGCAGTATTCAGGCTCTGATGTTCACTATTAAAGATTTTACA  
TGACCTCTTGGCTCTAATGTGTCATCAGTCAATTTTACTGTGATGATGTTCTCTTGGTCACT  
TATGCTTTGCTCAAAATGCACAGGAAATAGAATTGTGAGCATACTATTCTCTGATTTAATT  
TGATCTCCTCTTTCTGATAGTCTTAGTGTCTACATGTTGATTTTGTAGCTATATGTGCA  
55 ATGCATCTCTGCAGAGGGCAGGAAAAAGGCTTTCTCCACATGTGGTTCCTCATTTGACAGTGG  
TGGTTGTGTTCTATGGTCTCTACTCTTCATGTACATGCAGCCCAATTCCACTCACTTCTTT

GATACTGATAAAATGGCTTCTGTGTTTTACACTTAGTAATCCCATGCTTAACCCCTTGAT  
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAATTGA  
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPCALPTGGLLHPHQHTMMEIANVSSPEVFLVLFSTPRLSLETVLVIVLVFVMSILNGNI  
ILVSHDVLHLHPMPYFFLANLPFLDMSFTTISIVPQLLANLWGPQKTSYSGGCVVQFYFISHWLG  
ATBCEVLLATMSYDRAAIAICRPLHYTVIMHPQLCLGLALASWLGGLTTSVMGSTLTMLPLCG  
NNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLVPLGLLVSYGHIARAVLKRISAEGR  
10 KRAFNTCSSHVAVVSLFYGSIIFMYLQPAKSTSHSEQGKFIALFYTVTPALNPLIYTLRNEVKS  
ALRHMVLENCCGSAKGLAQI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCCAAGGTGGCCTTTTGCCCCACCCCCAGCATACAAT  
GATGGAAATAGCCAAITGTGAGTTCTCCAGAAGTCTTTGTCTCTCGGGCTCTCCACACGA  
15 CCGCTCACTAGAAACTGTCTCTTCATAGTTGTCTTGAGTTTTTACATGGTATCGATCTTGGG  
CAATGGCATCATCAATCTGGTCTCCCATACAGATGTGCACCTCCACACCACTATGTACTTCT  
TTCTTGCCAACTCCCGCTTCTGGACATGAGCTTCAACACGAGCATTTGCCACAGCTCTCG  
GCTAACTCTGGGGACACAGAAAAACCATAAGCTATGGAGGGTGTGTGGSTAGCTTCTAT  
ATCTCCCAATGGCTGGGGCAACCGAGTGTGTCTGTGGCCACCATGTCTATGACCGCT  
20 ACGCTGCCATCTGCAGGCCACTCCATTACACTGTCAATTATGCATCCACAGCTTTGGCTTGG  
CGTAGCTTTGGCTCTGTGGTGGGGGTCTGACCACGAGCATGGTGGGCTCCACGCTCACC  
ATGCTCTACCGCTGTGTGGGAACAAATGCATCGACCACTTCTTTGCGAGATGGCCCTCA  
TTATGCAACTGGCTTGTGTGGATACCAAGCTCAATGAGATGGAGATGTAAGCTGGCCAGCTT  
TGTCTTTGTGTCTGCCTCTGGGGCTCATCCTGGTCTCTACGGCCACATTGCCCGGGCCG  
25 TGTTGAAGATCAGGTGACGAGAAAGGGCGGAGAAAGGCACTTCAACACCTGTCTTCCACG  
TGGCTGTGGTGTCTGTGTTTTACGGGAGCATCATCTTATGATATCTCCAGCAGCCAGCAAG  
CACTCCCATGAGCAGGGCAAGTTCATAGCTGTCTTACACCGTAGTCACTCTGCGCTG  
AACCACCTATTACACCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGCACATGGTA  
TTAGAGAACTGTGTGGCTCTGACGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).

30 **AOLFR249 sequences:**

MKSQIEKSDLKYRAILLQKVTRMFLFWLILLVLSRLVVMGRGNSTEVTEFHLLGFGVQHEF  
QHVLFVILLIYVTSIGNIGMILLIKTDSRLQTPMYFFPQHLAFVDICYTSAITPKMLQSFTEEN  
NLITFRGCVIQLVYATFATSDCYLLAIMAMDCYVAICKPLRYPMIMSQTQVYIQLVAGSYIHGI  
35 NASVHTGTFSLSFCKSNKINHHFFCDGLPILALSCSNIDINILDVVFVFDLMTLVELVIFYSIYIM  
VTILKMSSTAGRKKSFSCTASHLTAVTIFYGTL SYMYLQPSNNSQENMKVASIFYGTVIPMLN  
PLIYSLRNKEKG (SEQ ID NO: 467).

ATGAAAGTCAAAATGAAAAAGTGACTTAAATATAGAGCCATTTTATTGCAAAAAGTC  
ACAAGGATGTCTGCTCTTTCTGGGTCTCTCTTGGGCTCTTGTGATCTTTGGTAGTCAT  
GGGTCGAGGAAACAGCACTGAAGTGACTGAATTCATCTTCTGGGATTTGGTGCCAAAC  
GAATTTACAGATGTCTCTTTCATTGTACTTCTTCTATCTATGTGACCTCCCTGATAGGAAA  
20 TATTGGAATGACTCTTATCTCATCAAGACCGATCCAGACTTCAAAACACCCATGTACTTTTTC  
CACAACTTTGGCTTTTGTGATATCTGTTATACTTCTGCTATCATCCCAAGATGCTCCAA  
AGCTTCAAGAAGAAAAATAATTGATAACATTTGGGCTGTGTGATACAACTCTTAGTCT  
ATGCAACATTTGCAACCACTGACTGTACTCTCTAGCTATTATGGCAATGAGTTGTTATGT  
45 TGCCATCTGTAAGCCCTTCGCTATCCCATGATCATGTCCCAACACGATCATCATCCAACTG  
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGTACATACAGGTTTTCATTTTCA  
CTGTCTCTCTGCAAGTCTAATAAAATCAATCACTTTTCTGTGATGGTCTCCCAATTTCTGC  
CCTTTGATGCTCCCAACTGACATCAACATCATCTAGATGTGTCTTTTGGGATTTGACAT  
TGATGTTCTAGTGTGGTCAATCTTTTCTTACATCTACATTAATGGTCACCATCCTGAAG  
ATGTCTTCTACTTGGGAGGAAAAATCCTCTCCCATGTGCTCCACCTCCACCTGACAGAG  
TAACCATTTTCTATGGGACACTCTTACATGTACTTACAGCCTCAGCTCAATAATTTCTAG  
GAGAAATAGAAAGTAGCCTCTATATTTATGGCACTGTTATTCCTGATGTGAATCCTTTAAT  
55 CTATAGCTTGAGAAATAAGGAAGGAAAAATAA (SEQ ID NO: 468).

**AOLFR250 sequences:**

MENQSSIEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNNLLIILAGSDLHLHTPMYFFLANLSFV  
DMGLTSSVTYKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLDSFLLAAMAYDRVYAICHPLCY  
STVMRPQVCALMLALCWVLTNIVALTHTFMLMARLSFCVTGELAHFFCDITPVKLKSCSDTHINE  
MMVFVLGGTVLIVPFLCIVTSYIHIVPAILRVTRGGVGKAFSTCSSHLCCVVCVFGYGLFSAYLCC  
PPSIASEEKDIAAAAAYTIVTPMLNPFYISLRNKMKGALKRFLSHRSIVSS (SEQ ID NO: 469).

ATGGAACCAACATCCAGCATTTCTGAAATTTTCTCCGAGGAATATCAGCGCCTCCAGAGC  
AACAGCAGTCCCTCTTCGGGAATTTCTCTGTGTATGTATCTTGTACCTTGACTGGGAACCTGC  
CTCATCATCTTGGCCATTGGCTCTGACCTGCACCTCCACACCCCATGTACTTTCTTGGC  
CAACCTGTCTTTGTGTACATGGGTTTAACGTCTCCACAGTTACCAAGATGCTGGTGAAT  
ATACAGACTCGGCATACACCATCTCCCTATACGGGTTGCCTCAGCGAAATGTATTTCTTTCT  
GATGTTTGGTGATCTAGACAGCTTCTCTGGCTGCCATGGCGTATGACCGCTATGTGGCC  
ATTGGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCAAGTCTGTGCCCTAAATGCTTGC  
ATTGTGCTGGGTCTTACCAATATCGTTGCCCTGACTCACACGTCTCTCATGGCTCGGTTGT  
CTTCTGTGTGACTCGGGGAAATGTCTCACTTTTCTGTGACATCACTCTGCTCCTGAAGCTG  
TCATGTTCTGACACCACATCAACGAGATGATGGTTTTGTCTGGGAGGCCACCTGACTCA  
TCGTCCCTTTTTATGCAATTGTCACTCTCATACATCCACATTTGTGCCAGCTATCCTGAGGGTC  
CGAACCCCTGGTGGGGTGGGCAAGGCCCTTTCCACTCGAGTTCACACCTCTGGGTTGTGT  
GTGTGTTCTATGGGACCCCTTCTAGTGCTACTGTCTCCCTCCCTCATTTGCTCTGAAGAG  
AAGGACATTGACAGCAGCTGCAATGTACACCATAGTGACTCCCATGTTGAACCCCTTTATCT  
ATAGCCTAAGGAACAAAGGACATGAAGGGGGCCCTAAGAGGGCTCTTCACTACAGGAGTA  
TTGTTCTCTTAG (SEQ ID NO: 470).

**AOLFR251 sequences:**

MENKNTWITDITLPRFQVGPALAILLCLGLFSAFYTLTLGNGVIFGHCLDCKLHTPMYFFLSHLA  
IVDISYASRNVYPMKMLTNLMNQESTISFFPCIMQTFLYLAFAHVECLILVMSYDRYADICHPLRY  
NILMSRWVCTVLAVASVWSFLLALVPLVLILRPLFCGPEHINHFCEILSVLKLACADITVLNQRV  
VIFAACVFILVGPLCLVLVSYLRILAILRISQSEGRKKAFTSCSSHLCCVVLFGFAIVTYMAPK  
SRHPEEQQKVLVSLFYSLFNPMLNPLIYSLRNAEVKGLRRALRKLRT (SEQ ID NO: 471).

ATGGAAGGCAACAAGACATGGATCAGACATACCTTGCCGCGATTCCAGGTTGGTCCA  
GCACTGGAGATTCTCTCTGTGGACTTTTCTTGCCCTTCTATACACTACCCCTGCTGGGGAA  
TGGGGTCACTCTTGGGATTATCTGCTGGACTGTAAAGCTTACACACCCATGTACTTCTCC  
TCTCACACCTGGCAATTGTGACATATCTATGCTTCCAACTATGCCCAAGATGCTGAGCG  
AATCTTATGAACAGGAAAGCACCATCTCCTTTTTTCCATGCATAATGCAACATCTTGT  
ATTGTGCTTTTGCTCAGTAGAGTGTCTGATTTTGGTGGTGATGTCTATGATCGCTATGCG  
GACATCTGCCACCCCTTACGTTACAATATCTCTCATGAGCTGGAGAGTGTGACTGTCTGG  
CTGTGGCTTCTGGGTGTTCAGCTTCTCTCTGGCTCTGGTCCCTTAGTGTTCATCTGAGG  
CTGCCCTTCTGGGGCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCCCTCAAGTT  
GGCTGTGCTGACACTGGCTCAACCAAGTGGTCACTCTTGCAGCTGCGGTGTTCATCTGT  
GTGGGGCACTCTGCTGTGTGTCTCTCTCTGCTGCTGCGCATCTGGCCGCCATCTTGAGGA  
TCCAGTCTGGGGAGGGCCGAGAAAGGCTTCTCCACCTGCTCTCCCACTTCTGGCTGGT  
GGACTCTTCTTGGCAGGCCATTGTCACTACATGGGCCCAAGTCCCGGCACCTGAGG  
GAGCAGCAGAAAGTTCTTCCCTGTTTTACAGCCTTTTCAATCCAATGCTGAACCCCTGA  
TATATAGCCTAAGGAATGCAGAGGTCAAGGGCGCCTCAGGAGGGGCACTGAGGAAGGAG  
AGGCTGACGTGA (SEQ ID NO: 472).

**AOLFR252 sequences:**

MLRANQTLGGDFLLGIFSQISHPGRCLLIFSIPLMAVSWNITLILLIHIDSSLHTPMYFFINQLSL  
IDLTYISVTYPMKMLVNQLAKDKTISVLGCGTQMYFYQLGGAECCLLAAMAYDRVYAICHPLR  
YSVLMHVRVCLLLASGCFWFGVSDGFMFLTPIAMSFPCRSHIEIQHFCEVPAVLKLSGSDTSLY  
KIFMYLCCVIMLLIPYTVISVSYYYIILTHIKMNSVEGRKKAFTTCSHITVVSLEYGAAYNYML  
PSSYQTPKEDMMSSFFYTILTPVLNPIIYFSFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

ATGCGGCTGGCCAACAGACCCTGGGTGGTGACTTTTCTGTTGGGAATCTTCAGCCAGA  
TCTCACACCCTGGCCGCTCTGCTTGCTTATCTTCAGTATATTTTGAATGGCTGTGCTTGG  
AATATTACATTGATACTTCTGATCCACATTGACTCCTCTCTGCATACITCCCATGTACTTCTT  
TATAAACCAAGCTCTCACTCATAGACTTGACATATATTTCTGTCAGTGTCCCAAAATGCTG  
5 GTGAACCAAGCTGGCCAAGACAAGACCATTCTGGCTCCTTGGGTGTGGACCCAGATGTAC  
TTCTACCTGCAAGTTGGGAGGTGACAGAGTGTGCTCTTACGCCGCCATGGGCTATGACCGCT  
ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC  
CTGGCATCAGGCTGCTGGTTTGTGGGCTCAGTGGATGGCTTCATGTCATCCCATCCGCA  
TGAGCTTCCCCTTCTGCAGATCCCATGAGATTACAGCACTTCTCTGTGAGGTCCTGCTGTT  
10 TTGAAGCTCTCTGCTCAGACACCTCACTTTACAAAGATTTTCATGTACTTGTGCTGTGTCAT  
CATGCTCCTGATACCTGTGACGGTCAATTTACAGTGTCTTACTACTATATCATCTCCACCATCC  
ATAAGATGAACCTGTGAGGGTCGGAAGAAAGCCCTCACCCAGCTGTCTCCCATCAATTAC  
AGTGTTCAGCCCTTCTATGGAGTGTCTATTTACAACACATGCTCCCAAGCTCCATACCAA  
ACTCCTGAGAAAGATATGATGTCATCCTTTTCTACACTATCCTTACAGCTGTCTTGAATCC  
15 TATCATTTACAGTTTCAGGAATAAGGATGTACAAAGGGCTTTGAAAAAATGCTGAGCGT  
GCAGAAACCTCCATATTA (SEQ ID NO: 474).

#### AOLFR253 sequences:

MTFFSSGGNCEPVMCSGNQTSQNQTASTDFTLTGLFAESKHAALLYTVTFLLFLMALTGNALL  
20 ILLIHSEPRLHTPMYFFISQLALMDLMLYLCVTPKMLVGQVTGDDTISPSGCGIQMFFHLILAG  
AEVFLLAAMAYDRYAACVCRPLHYPLLMNQRYCQLLVSAWVLMVMDGLLLTPITMSFFPQCS  
RKILSFFCETPALLKLSGSDVSLYKMLTYLCCMLMLTPIMVISSSYTLILHLIHRMNSAAGRRKA  
LATCSSHMIIVLLFGASFYTYMLRSSYHTAEQDDMMVSFAFYTIFPVLNPLIYSLRNKDVTAL  
RSMMQSRMNQEK (SEQ ID NO: 475).

ATGACATTTTCTTCTCAGGGGGAACACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT  
CTCAGAACTAAACAGCAAGCACTGATTTACCCCTCACGGGACTCTTGTGTGAGAGCAAGCA  
TGCTGCCCTCCTCTACACCGTGACCTTCTTCTTTCTGTATGGCCCTCACTGGGAATGCC  
TCTCATCTCTCTCATGCACTCAGAGCCCGCTCCACACCCCATGTACTTCTTCATCAGC  
30 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCAAGATGCTTGTGGGCG  
AGGTCACTGGAGATGATACCAATTTCCCGCTCAGGCTGTGGGATCCAGATGTTCTTCCACT  
GACCTGGCTGGAGCTGAGGTTTTCCTCCTGGCTGCCATGGCCTATGACGATATGCTGCT  
GTTTGACGACCTTCTCCATTACCCACTGCTGATGAACAGAGGGTGTGCCAGCTCCTGGTGT  
35 CAGCGTCTGGGTTTGGGAATGGTTGATGGTTTGTGCTCACCCCCATACCATGAGCTT  
CCCTTTTGCCAGTCTAGGAAATCCTGAGTTTCTGTGAGACTCCTGCCCTGCTGAAGC  
TCTCTGCTCTGACGTCTCCCTCTATAAGATGCTACGTAACCTGTGCTGCATCTCATGCTT  
CTCACCCCATCATGTTGCTATCCAGCTCATACACCTCATCTCATCTCATCCACAGGAT  
GAATTTCTGCCCGCGCCGAGGAAGGCCCTTGCCACCTGCTCCTCCACATGATCATAGTGT  
CTGCTGCTCTTCGGTGCTTCTCTTACACCTACATGCTCCGAGTCTCTACACCAAGCTGA  
40 GCAGGACATGATGGTGTCTGCTTTACACCATCTTCACTCCTGTGCTGAACCCCTCATTT  
ACAGTCTCGCAACAAAGATGTCAACAGGGCTCTGAGGAGCATGATGCAGTCAAGAATGA  
ACCAAGAAAAGTAG (SEQ ID NO: 476).

#### AOLFR254 sequences:

MTNTSSSDFLLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI  
45 MDTLFICTTYPKLLADMVSKEKIIIFVACGIQFLYLTIMGSEFFLLGLMAYDCYVAVCNPLRYP  
VLMNRKKCLLLAAGAWFGGSLDGLLTPITMNPVYCGSRINHHFCEPVLKILACADTSLEYT  
LMYICCVLMLLIPISISYSYSLILLTIHRMPSAEGRKKAFTTCSHLLTVVSIFYGAAFYTVLPQS  
FHTPEQDKVVSFAFYTIVTPMLNPLIYSLRNKDVGIAFKKVACSSAQKVATSDA (SEQ ID NO:  
50 477).

ATGACGAACACATCATCTCTGACTTACCTCCTGGGGCTTCTGGTGAAACAGTGAAGGCTG  
CCGGGATGTTATTTACAGTGATCCTTGTGTTTCTTGGGGGCGGTGATGCAAAATTTGGT  
CATGATATTTCTGATTCAGGTGGACTCTCGCTCCACACCCCATGACTTCTTCTGCTCAGTC  
55 AGCTGTCCATCATGGACACCTTTTTCATCTGTACCAGTGTCCCAAACTCTGGCAGACAT  
GGTTTCTAAAGAGAAGATCATTTCTTTGTGGCTGTGGCATCCAGATCTTCTCTACCTG

ACCATGATTGGTTCCTGAGTCTTCTCTCTGGGCTCATGGCCTATGACTGCTACGTGGCTGT  
CTGTAAACCTCTGAGATACCCAGTCTGATGAACCGCAAGAAGTGTCTTTTGGCTGGCTGCT  
GGTGGCTGGTTTGGGGGGCTCCCTCGATGGCTTTCTGCTACTCCCATCCACCTGAATGATGCC  
CTTACTGTGGCTCCCGAAGTATCAACCATTTTTCTGTGAGATCCCAAGCAGTTGTCTGAAACT  
5 GCTGCTGTGCAGACGCTCCTTGTATGAAACTCTGATGTACATCTGCTGTGCTCTGATGTG  
CTCATCCCCATCTCTATCATCTCCACTTCTACTCCCTCATCTGTGTAACCATCCACCGCAT  
GCCCTCTGCTGAAGGTGCGAAAAAGGCCCTCACCACTTGTCTCCCACTTGACTGTAGTIT  
AGCATCTTCTATGGGGCTGCTTCTACACATACGTGCTGCCCCAGTCTTCCACACCCCG  
AGCAGGACAAAGTAGTGTACGCTTCTATACCATTTGTCACGCCCATGCTTAATCTCTCAT  
10 CTACAGCCTCAGAAACAGGACGTACAGGGCATTAAGGGCATTTAAACAGGTATTTGCATGTGTCTCA  
TCTGCTCAGAAAGTAGCAACAAGTGATGCTTAG (SEQ ID NO: 478).

#### AOLFR255 sequences:

MEQSNYSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKILIHDSRLHTPMYFLLSQLS  
15 IRLDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGEFFLLGLMSYDRYVAICNPLH  
YPVLMSRKICWLVIAAAWLGGSIDGFLTPVMTQFPFCAAREINHFCEVPAILLKSLCTDTSAY  
ETAMVYCCIMMLLIPFSVISGSYTRILITYRMSAEGRGKAVATCSSHMVVVSLFYGAAMYT  
YVLPHSYHTPEQDKAVSAFYITLTPMLNPLIYSLRKNVDVTGALQKVVGRCVSSGKVITF (SEQ  
ID NO: 479).

ATGGAGCAGAGCAATTATTCGGTGTATGCCGACTTTATCTCTTGGGTTTGTTCAGCAACG  
CCCGTTTCCCTCGGCTTCTCTTGCCCTCATCTCTGGTCTTTTGTACCTCCATAGCCAGC  
AACGTGGTCAAGATCATTTCTATCCACATAGACTCCCGCTCCACACCCCATGACTTCTCT  
GCTCAGCCAGCTCTCCCTCAGGGACATCTGTATATTTCCACCAATGTGCCCCAAAATGCTG  
25 TGTGACAGGTGATGAGCCAGAGAGGCCATTTCTTTGCTGGATGCACTGCCCAACATCTCC  
TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCTAGGACTCTGCTATGATGCTGCTACAT  
GTAGCCATCTGCAACCTCTGCACTATCTGTCTCTATGAGCCGCAAGATGCTGCTGGTGA  
TTGTGGCGGCAGCCTGGCTGGGAGGCTCATCGATGTTTCTGTCTACCCCCGTCAACAT  
30 GCAAGTCTCCCTTCTGTGCTCTCTGGGAGATCAACCACTTCTCTGCGAGGTGCTGCGCCCTC  
TGAAGCTCTCTGCGAGCACATCAGCCTACGAGCAGCCATGTATGTCTGCTGTATTAT  
GATGCTCTCATCCCTTCTCTGTATCTCCTGGCTCTTACACAGAATTTCTATTACTGTTT  
ATAGGATGAGCGAGCAGAGGGGAGGGGAAAGGCTGTGGCCACCTGCTCCCTCACACATGG  
TGGTTGTGAGCCTCTCTATGGGGCTGCCATGTACACATACGTGCTGCTCATTTCTAACCA  
35 ACCCTGAGCAGGACAAAGCTGTATCTGCTTCTACACCATCTTACTCCCATGCTCATCT  
CACTCATTTACAGCCTTAGGAACAAGGATGTACAGGGGCCCTACAGAAGGTTGTGGGGA  
GGTGTGTGCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 480).

#### AOLFR256 sequences:

MGGKQPWVFTEFILVGFQVGPALAILLGLFSVFTLLLNGVIFGHCILDSKLHTPMYFFLSHL  
40 AIIDMSYASNNVPKMLANLMNQKSTISFVPCIMQTFLYLAFVTECLILVMSYDRYVAICHPF  
QYTVMSWRVCTILASTCWIISFLMALVHITHILRPFCGPKINHFICQIMS VFKLACAGPRLNQ  
VVLVAGSAFIVEGPLCLFLVSNLHLSRLEDPVMGRAADRLTLPAPSHLCMVGLFLGSTMVM  
YMAPKSRHPPEEQKVLFLSFLNPMNLPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:  
481).

ATGGGAGGCAAGCAGCCCTGGGTCACAGAATTCATCTGGTGGGATTCCAGGTTGGTCCA  
GCACCTGGCGATTCTCCTCTGTGGACTTCTCTGTCTCTATACACTCACCTGCTGGGGAA  
TGGGGTCACTTTTGGGATTATCTGCCTGGACTCTAAGCTTACACACCCATGTACTTCTCC  
TCTCACACCTGGCCATCATTGACATGTCTATGCTTCCAAATGTTCACCAAGATGTGGC  
50 AAACCTAATGAACACGAAAAAGCACCATCTCCTTTGTCTCATCATTAATGCAGACTTTTTG  
TATTTGGCTTTTGCTTTACAGAGTGCCTGATTTTGGTGGTGATGTCTATGATAGGATGTG  
GGCCATCTGCCACGCTTTCCAGTACACTGTCTCATGAGCTGGAGAGGTGTCACGAGTCTG  
GCCTCAACATGCTGGATAATTAGCTTCTCATGGCTCTGGTCCATATAACTCATATTCTGAG  
GCGGCTTTTGTGGGCCACAAAAGATCAACCACTTTATCTGTCAAAATCATGTCCGATTTCA  
55 AATTGGCTGTGCTGGCCCTAGGCTCAACAGGTGGTCTATATGCGGGTTCTGCGTTCAT  
CGTAGAGGGGCGCTCTGCTGGAGCTGGTCTCCAACCTGCACATCTGTGCGCCATCTT

GAGGATCCAGTAATGGGGAGGGCCGAGACCGACTTACTCTTCTGCTCCTTCCCACTTT  
GCATGGTGGGACTCCTTTTTTGGCAGCACCATGGTCACTGTACATGGCCCCCAAGTCCCGCCA  
CCCTGAGGAGCAGCAGAAGGTCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATGCTGAAC  
CCCTTGATCTACAGCCTGAGGAACGAGAGGTCAAGGGTGCCTGAAAGAGTGTGTGG

5 AAACAGAGATCAAAGTGA (SEQ ID NO: 482).

# **AOLFR257 sequences:**

MESNQTWITEVILLGFQVDPALELFLFGFLLFYSYLLMGNGIHLGLIYLSRLHTPMYVFLSHL  
AIVDMSYASSTVPKMLANLVMHKKVISFAPCILQTFLYLAFATECLILVMMCYDRYVAICHPL  
QYTLIMNWRVCTVLASTCWIFSLLALVHITLILRLPFCGPKQINHFQIMSVFKLACADTRYL  
QVVFLFAGSAFVLVGLCLVLSYLHILVAILRIQSGEGRKAFSTCSSHLVVGFLFSGSAIVMVM  
APKSSHSQERRKILSLFYSLFNPLNPLIYSLRNAEVKGALKRVLWKQRSM (SEQ ID NO: 483).

10

ATGGAAGCAATCAGACCTGGATCACAGAAGTCATCTGTTGGGATTCCAGGTGGACCCA  
GCTCTGGAGTTGTCTCTCTTTGGGTTTTTCTTGCTATTCTACAGCTTAACCTGATGGGAAA  
TGGGATTATCTGGGGCTCATCTACTTGGACTCTAGACTGCACACACCCATGTATGTCTTC  
CTGTGCACACTGGCCATTGTGGACATGTCTTATGCTCGAGTACTGTCCCTAAGATGCTAG  
CAAACTCTGTGATGCACAAAAAAGTCATCTCCTTTGCTCCTTGCTACTACTCAGACTTTTTTG  
TATTTGGCGTTTGTCTATTACAGAGTGTCTGATTTTGGTGTATGATGTGCTATGATCGGTATG  
TGGCAATCTGTCACCCCTTGCAATACACCTCATTATGAAGTGGAGAGTGTGCACGTCTCT  
TGCTCAAACTTGCTGGATATTTAGCTTTCTCTTGGCTCTGGTCCATATTACTCTTATCTGA  
GGCTGCTCTTTTGTGGGCCACAAAAAGATCAACCACTTTTTCTGTCAAACTCATGTCCGTAITTC  
AAATTTGGCTGTGTGCTGACACTAGGCTCAACCAAGTGGTCTATTTCGGGGTCTCGCGTTCA  
TCTTAGTGGGGCGGCTCTCGCTGGTGTGCTCTCTACTTGACATCTCGGTGGGCCATCTTG  
AGGATCCAGTCTGGGGAGGGCCGAGAAAGGCTCTCTACTGCTCTCTCCCACTGCTGCG  
TGGTGGGCTTTCTTTTGGCAGCGCCATTGTCACTGTACATGGCCCCCAAGTCAAGCAATTC  
TCAAGAACGAGGAAGATCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATCTCAACCC  
CTCATCTACAGCCTTAGGAATGCAGAGGTGAAAGGGGCTCTAAGAGAGTCTCTTGGAAA  
CAGAGATCAATGTGA (SEQ ID NO: 484).

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# **AOLFR259 sequences:**

MGDNQSRVTEFILVGFQLSVEMEVLLFWIFSLLYLFSLLANGMILGLICLDPLRLTPMYFFLSHL  
AVIDIYYASSNLLNMLENLVKHKKTISFISCIMQMALYLTFAAAVCMILVMSYDRFVAICHPL  
HYTVIMNWRVCTVLAITSWACGFSALINLJLLRLPFCGPQEVNHFFGEILSVLKLACADTWIN  
EIFVFAGGVFLVGLSLMLISYMRILLAILKIQSKEGRKAFSTCSSHLVVGLYFGMAVMVY  
LVPDNSQRQKQKILTLFYSYLFNPLNPLIYSLRNAQVKGALYRALQKRTM (SEQ ID NO:  
485).

35

ATGGGGGCAACCAATCAGGGTCACAGAATTATCTGTTGGATTCCAGCTCAGTGTG  
GAGATGGGAAGTGTCTCTCTGGATCTTCCCTGTTATATCTCTTCAAGCCTCTCTGGCAAA  
TGGCATGATCTTGGGGCTCATCTGTCTGGATCCAGACTGCGCACCCCATGTACTTCTTC  
TGTCACACTTGGCCGTCATTGACATATACTATGCTTCCAGCAATTTGCTCAACATGTCTGGA  
AAACCTAGTGAACACAAAAAACTATCTGTTTCATCTCTTGCAATATGAGATGGTCTTTG  
TATTTGACTTTTTGCTGCTGCACTGTGATGATTTTGGTGGTGTATGCTCTATGACAGATTTGT  
GGGATCTGCGCATGCCCTGCAATTACACTGTCACTATGAACCTGGAAGAGTGTGCACAGTACTG  
GCTATTACTTCTGGGCACTGTGGATTTTCCCTGGCCCTCAATAACTTAATCTCTCTCTAAG  
GCTGCCCTCTGTGGGCCCCAGGAGGTGAACCACTTCTCGGTGAAATCTGTCTGCTCCT  
AACTGGCCTGTGCAGACACTGGATTAATGAAATTTTGTCTTTGCTGGTGTGTGTTTG  
TCTTAGTCGGGCCCTTTCTTGTATGCTGATCTCTACATGCGCATCTCTTGGCCATCTCTG  
AAGATCCAGTCAAAGGAGGGCCGCAAAAAAGCCTTTTCCACCTGCTCTCTCCCACTCTGTG  
TGGTTGGGCTTTACTTTGGCATGGCCATGGTGGTTTACCTGGTCCGACCAACAGTCACAGC  
ACAGAAAGCAGCAAAAAATCTCACCTGTTTTACAGCCTTTTCAACCCATGTCTGAACCC  
CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCCTTATACAGAGCACTGCAGAAA  
AAGAGACCATGTGA (SEQ ID NO: 486).

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**AOLFR24B sequences:**

MPSINDTHFYPPFFLLLGIPGLDTHLHWISFPFCIVYLIAVGNMTILFVIKTEHSLHQPMFYFLAM  
LSMDLGLSTSTPKMLGIFWNLQEIFSGGCLLQMFHMFMTGMEIVLVVVMAYDREVAICNP  
LQYTMILTNKTISILASVVVGRNLVLVTFPFFLLRLPFCGHNIVPHTYCEHRGLAGLACAPIKN  
5 IYGLMVISYIIVDVLIIASSYVLLRAVFLRPSQDVRCLKAFNCTCGSHVCMVLCFYTPAFFSMTH  
RFGQCNPHYIHILLANLYVVPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCTCTCTATCAATGACACCCACTTCTATCCCCCTTCTCTCTCTGCTAGGAATAACAGG  
ACTGGACACCTTATACATATCTGGATTCTTCCCAATCTGTAATGTGTACCTGATTGCCATGT  
10 TGCGGGAATATACCACTTCTCTTTGTGATCAAAACTGAACATAGTCTACACAGCCAGCCATGTT  
CTACTTCTGGCCATGTTGTCTATGATTGATCTGGGCTGTCCACATCCCATATCCCCAAAA  
TGCTAGGAATCTCTGGTTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTTCAGAT  
GTTCTTTATTCACATGTTTACAGGCATGGAGACTGTTCTGTGGTGGTCATGGCTTATGACC  
GCTTTGTTGCCATCTGCAACCCCTCTCCAGTACACCATGATCCTCACCAATAAACCATCAG  
15 TATCCTAGCTTCTGTGGTTGTGGGAAGAAATTTAGTCTTGTGAACCCCATTTGTGTCTTCA  
TTCTGCGTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG  
TCTGGCCGGGTGTGGCTGTGCACCCATTAAAGATCAACATAATCTATGGGCTCATGGTGATT  
TCTTATATTATTGTGGGATGTGATCTTAATTGCCCTCTTCTTATGTGCTTATCCTTAGAGCTGT  
TTTTCGCCTCCCTCTCAAGATGTCCGACTAAAGGCCTTCAATACCTGTGGTTCTCATGTCT  
20 GTGTTATGCTGTGCTTTTACACACCAAGCATTTTTTCTTTTATGACACATCGTTTGTGGCAA  
AAACATTCGCCACTATATCCATATCTTTTGGCTAACCTGTATGTGGTGTGCCAAGTCCCT  
TAACCTGTCAATTTATGGAGTCAGGACCAAGCATCCGAGAGCAAAATGTGAAAAATATTT  
GTACAGAAAGAATAA (SEQ ID NO: 488)

**AOLFR33B sequences:**

MLHTNNTQFHPSTFLVVGVPGLDGVHVGWIGFPFFAVYLTALLGNIIILFVIQTEQSLHQPMFYFL  
AMLAGTDLGLSTATIPKMLGIFWNLGEIAFGACITQMYTHICTGLSESVLTVTGIDRYIAICNP  
LRYSMILTVIALGIVHVRILVFPFPTLTLRLPCFVRIHPHTYCEHMGKALACASINPV  
30 GLIAFSVGYIDISVIGFSYVQILRAVFLPAWDARLKALSTCGSHVCMVLAFLYLPALFSFMTHRF  
GHNIPHYIHILLANLYVVPALNSVIYGVKTKQIREQVLRILNPKSFWFHDFDKRIFHNNSVRQ  
(SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTACCCTTCCACCTTCTCTGTAATGGGGGTCCAG  
GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCTTCTTTGCGGTGTATCTAACAGCCCT  
35 TCTAGGGAACATCATTATCCTGTTTGTGATACAGACTGAACAGAGCCCTCCACACCCATG  
TTTTACTTCTAGCCATGTGTGGCCGGCACTGATCTGGGCTTGTCTACAGCAACCAATCCCA  
AGATGTCCGGGAATTTTTCTGGTTTAATCTTGGAGAGATTGCAATTTGGTGCCTGCATCACACA  
GATGTATACCATTCATATATGCACTGGCTGGAGTCTGTGGTACTGACAGTCAAGGGCATA  
GATCGCTATATTGCCATCTGCAACCCCTCGAGATATAGCATGATCCTTACCAACAAGGTAA  
40 TAGCCATTCTGGGCATAGTCATCAATTGTCAGGACTTTGGTATTTGTGACTCATTCACATTT  
CTCACCCCTGAGATTGCCTTTCTGTGGTGTCCGGATTATCCCTCATACCTATTGTGAACACAT  
GGGCTTGGCAAAGTTAGCTTGTGCCAGTATTAATGTTATATATGGATTGATTGCTTCTCA  
GTGGGATACATTGACATTTCTGTGATTGGATTTTCTATGTCCAGATCCTCCGAGCTGTCTT  
CCAATCTCCAGCCTGGGATGCCCGGCTTAAGGCACCTCAGCACATGTGGCTCTCACGCTGTG  
45 GTTATGTGGCTTCTACCTGCCAGCCCTCTTCTCTCATGACACACCGCTTTGGCCACAA  
CATCCTCATTCATCACCATCTCTTCTGGCCATCTGTATGTGGTTTCTTCCCTCTGCTCTTA  
ACTCTGTTATCTATGGGGTCAAAACAAAACAGATAAGAGAGCAGGTACTTAGGATCTCA  
ACCTTAAAGCTTTTGGCATTTTGACCCCAAGAGGATCTCCACAACAATTCAGTTAGACA  
ATAA (SEQ ID NO: 490)

**AOLFR112B sequences:**

MKNKTVLTFEILLGLTDVPELQVAVFTFLFLAYLLSILGNLTILITLLDSHLQTPMYFFLRNFSF  
LEISFTNIFPRVLISITGNKSISFAGCTQYFFAMFLGATEFYLLAAMSVDYRVYAIKPLHYTTI  
55 MSSRICQLIFCSWLGGMLAIPTITLMSQQDFCANRLNHYFCDYEPLELSCDSTLIEKVVF  
VASVTLVTVTLVVLVSYAFIITILKLPSAQQRKAFSTCSSHMVISLSYSGCMFMYNPSAKEG  
DTFNKGVALLITSVAPLLNPFYITLNRNQVQKQPFKDMVKLLNL (SEQ ID NO: 491)

ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCCTGAAC  
 TCCAGGTGGCAGTTTTACCTTTCTTTTCTTGCATTTTACTCAGCATCCTTGGAAAACTCG  
 ACTATCTCTACTCTCCAGTCTTGGTGGACTCCACCTTCAGACTCCCATGATTCTTCTTCCG  
 5 GAACCTTCTCCTCTTGGAAATTTCCCTTACAAACATCTTCACTCAAGGGTCTGATTAGCA  
 TCACAACAGGGAACAAGAGTATCAGCTTTGCTGGCTGCTTCACTCAGTATTTCTTTGGCAT  
 GTTCTTTGGGGCTACAGAGTTTTACCTTCTGGCTGCCATGTCTATGACCGCTATGTGGCC  
 ATCTGCAAAACCTCTGCATTACACCACCATCATGAGCAGAGAATCTGCATCCAGTGATT  
 10 TCTGCTCTTGGCTGGGTGGGCTAATGGCTATTATACCAACAAATCACCCCTGATGAGTCAGCA  
 GGCATTTTGTGATCCAAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTTCTGGAA  
 CTCTCATGTTCAGACACAAGCCTCATAGAGAAGGTGTCTTCTTGTGGCATCTGTGACCC  
 TGGTGGTCACTCTGTGTCTAGTGATTCTCTCTATGCATTCAATACAGACTATTCTGAAG  
 CTCCCCCTCGCCCAACAAAGGACAAAAGCCTTTTCCACATGTTCTTCCACATGATTGTCAT  
 15 CTCCCCTCTCTTACGGAAGCTGCATGTTTATGTACATTAATCCCTCTGCAAAAGAAGGGGAT  
 ACATTCAACAAGGGAGTAGCTCTACTCTACTTCACTTCACTTGTCTCCTTGTGAAACCCCTTAT  
 TTACACCTTAAGGAACCAACAGGTAAAACAACCCCTCAAGGATATGGTCAAAAAGCTTCT  
 GAATCTTTAA (SEQ ID NO: 492)

# **AOLFR130B sequences:**

20 MEKGNQTAPESEFILGFDHNLQYLLFTIFFLYICTLGGNVFHVVIADSHLHTPMYYFLGNL  
 ALIDICVTITNVNQPMQMHLLSEKKIJSYGGCVTLQFAFFVFGSECLLAAAMAYDRYIAICKPLR  
 YSFIMNKALCSWLAAASCTWCGFLNSVLHTVLTFPLFCFNGNQINFYCDIPPLLLSCGDTSPLN  
 LALLSIGILISWTFPLCIILSYLYIISTILRIRSSEGRHKAFSTCASHLLIVLYYGSIAIFYVRPISSYS  
 LEKDRLISLVISVVTPLMPNVPVIYTLRNDIKEAVKAIGRWQPPVFFSSDI (SEQ ID NO: 493)

25 ATGGAAGGAAAGAATCAAAACAGCTCCATCTGAATTTCATCATCTTGGGGTTCGACCACCTGA  
 ATGAATTGCAGTATTACTCTTACCATCTTCTTCTGACCTACATATGCACCTTAGGAGGC  
 AATGTTTTTATCATTTGTGGTGACCATAGCTGATTCACCACTACACACACCCATGTATTATT  
 CCTAGGAAATCTTGGCCTTATTGACATCTGCTACACTACTACTAATGTCCCCAGATGATG  
 30 GTGCATCTTCTGTCAGAGAAGAAATCATTCTCTAGGAGCTGTGTGACCCAGCTCTTTG  
 CATTCACTTTCTTTGTTGGCTCAGAGTGTCTCCTCTGGCAGCAATGGCATATGATCGATAT  
 ATTGCTATCTGTAAGCCGTTAAGGTACTCATTTATTATGAACAAGGCCCTGTGCAGCTGGT  
 TAGCAGCCTCATGTGGACATGTGGGTTTCTCAACTCAGTGTGACACCCGTTCTGACCTT  
 CCACCTGCCCCTTCTGTGGTAACAATCAGATCAATTATTTCTTCTGTGACATACCTCCCTTGC  
 35 TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAACCTGGCTTGTCTGTCATTGGGATCCTC  
 ATAAGCTGGACTCCTTCTCTGTGCATCATCTTCTTCTACCTTTACATCATCTCCACCATCTC  
 GAGGATCCGTTCTCTGAGGGGAGGCACAAAGCCTTTTCCACCTGTGCCCTCCCAAGCTGTC  
 ATTGTTATCTCTATTATGGCAGTGCTATCTTCACTGATGTGAGGCCCATCTCATCTTACTC  
 TCTAGAGAAAGATAGATTGATCTCAGTGCTGTATAGTGTGTGCACACCCATGCTGAATCT  
 40 GTAATTTATACGCTAAGGAATAAGGACATCAAAGAGGCTGTGAAGGCCATAGGGAGAAAG  
 TGGCAGCCACCAGTTTTTCTTCTGATATATAA (SEQ ID NO: 494)

# **AOLFR142B sequences:**

45 MARKDMAHINCTQATEFILVGLTDHQLKMPFLVFLFSIYLVVGNLGLILLIRADTSLNTPM  
 YFFLSNLAFVDFCYSSVITPKMLGNFLYKQNVISFDACATQLGCFLTFMISESLLASMAVDYRY  
 VAICNPPLLYMVMTPGICQLVAVPYSSYFLMALFHTILTFLRLSYCHSNVNHFYCDMPLLRL  
 TCSDRFRQQLWFACGIMFISSLLIVFVSYMFHISAILRMHSAEGRQKAFSTCGSHMLAVTFYF  
 TLIFMYLQPSSSHALDTDKMASVFYTVIHPMLNPLIYSLQNKEVKEALKKIHNKN (SEQ ID NO:  
 495)

50 ATGGCCAGAAAAGATATGGCTCATCATTAATGGCACCCAGGCGACAGAGTTTTATTCTTGTGG  
 GCCTCACAGAAACATGAGAGTTGAAGATGCCCTCTTGTGCTATTCTTATCCATCTACCTC  
 TTCACAGTGGTAGGCAACTTGGGTTTGATCTTACTCATTAGAGCGGATACAAGTCTCAACA  
 CACCAATGTACTCTTCTTAGCAACCTAGCTTTTGTGGATTCTGTCTACTCTCTGTCATT  
 55 ACACCCAAAATGCTTGGGAATTTCTGTGACAAAACAAATGTTATATGCTTTGATGATGTG  
 CTACTCAACTGGGGTGCTTCTCACTTCAATGATATCAGAACTCTTGTACTTGGCTTCCATG

GCCTATGACCGATATGTGGCCATTGTGAACCCCTCTATTGTATATAGTTTGAATGACTCCAG  
 GAATCTGCATTCAACTGTGTAGCAGTTCCTTATAGCTATAGCTTCCTAAATGGCACTATTTCAC  
 ACCATCTCACCCTCCGCTCTCCTATTGCCACTCCAACTTGTCAAAACCACTTTCTATTGTGA  
 TGACATGCTCTCTCCACGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT  
 5 GCGCTGTGCTGGTATCATGTTCACTTCTCCCTTCTGATTGTCTTTGTCTCTCACTATGTTCACT  
 ATTTCTGCCATCTCTGAGGATGCATTACAGTCTGAGGGAAGACAGAAAGGCTTTCTCGACGTGTG  
 GCTCTCACATGCTGCGAGTACCAATATTCTATGGGACCCCTATTTTATGTACTTACAGCTCT  
 AGCTCTAGCCATGCGCTTGACACAGACAAGATGGCCCTGTCTTCTACACAGTGTATCATTC  
 CCATGTTGAATCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA  
 10 AATCATTTATCAATAAAAACCTAG (SEQ ID NO: 496)

# **AOLFR171C sequences:**

MAEVNIIIVTVFLKGITNRPQLQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYFYLSHL  
 AFVDLCYSSAITPKMMVNFVVERNTIPFHACATQLGCFLTFMITECFLLLASMAVDYVIAICSP  
 15 HYSTLMSRRVICQVAVPYIYSLVALFHVTITFRLTYCGPNLINHFYCDLPLFALS CSDTHMK  
 EILFAFAGFDMISSSSIVLTSYIFIIAAILRIRSTQGQHKAISTCGSHMVTVTIFVYGLIFMYLPQS  
 NHSLDIDKMASVFYTVVIMPLNPLIYSLRNKEVKDASKKALDKGCENLQILTFLKIRKLY (SEQ  
 ID NO: 497)

20 ATGGCTGAAGTTAATATCATTTATGTCACGTATTTCATTCTGAAAGGAATTACCAACCGGC  
 CAGAGCTTCAGGCCCCGTGCTTTGGGGTGTTTATAGTATCTATCTGGTCACAGTGTCTGGG  
 CAATCTTGGGTTGATTACTTTAATCAAGATTGATACCTGACTCCACACACCTTATGCTACTT  
 TCTCAGCACTCGCTGGCTTTGTTGACCTTTGTTACTCCTTGCTATACACCGAAGATGATG  
 GTGAATTTGTTGTGGGAACGCAACACCACTTCCCTTCCATGCTTTGTGCAACCAACCTGGGTT  
 25 GTTTTTCACCTTCATGATCACTGAGTGTTTCTCTAGCCCTCATGCGCTCAGGATTTGAT  
 GTGCGCATCTGATGCCCTGCATTATTCACACTGATGTCAAGAAGAGTCTGCATTCAAC  
 TGGTGGCAGTTCCATATATATACAGCTTCCCTGGTGTGCCCTCTCCACACCGCTTATCACTTC  
 CGTCTGACTTACTGTGGCCCAAACTTAATTAACCATTTCTATGTGTATGACCTCCCCCTCTT  
 AGCTCTGCTCTGCTCAGACACACATGGAAGGAAATCTCGATATTGTCCCTTTGCTGGCTTT  
 30 GATATGATCTCTTCTCTTCCATTGCTCACCCTCACCCTCATCTTATATTGCGCGTATCTCTA  
 AGGATCCGCTCTACTCAGGGGCAACACAAAGCCATTTCCACCTGTGGCTCCCATATGGTGA  
 CTGTCACTATTTCTATGGCACACTGATCTTTATGTACCTACAGCCCAAAATCAAACTCACTCC  
 TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGGTGTATGCCCATGTTAAACCCCC  
 TAATCTATAGCTAAGGAACAAAGAAGTGAAAAGATGCCTCAAAGAAAGCTTTGAGTAAAG  
 35 GTTGTGAAAACCTACAGATATTAACATTTTAAAAATAAGAAAACCTTTATTA (SEQ ID NO:  
 498)

# **AOLFR225B sequences:**

MKNRTMFGEFILLGLTNQPELQVMIFIFLFTYMLSILGNLTIITLTLDDPHLQTPMYFFLNRFS  
 LEISFTSIFPRFLTSMITGNKVISFAGCLTQYFFAIFLGADEFYLLASMSYDRYVIAICKPLHYLTI  
 40 MSSRVCIQLVFCSWLGGFLAILPPIILMTQVDFVCVSNLNHYCYDGPLVELACSDTSLLELMVI  
 LLAVVTLMTVLVLSYTYIIRITILRIPSQQRTKAFSTCSSHMIVLSYSGCMFMFYNPSAKE  
 GGFANKGIAVLITSVTPLLNPFHYTLRNQVQKQAFKDSVKKIVKL (SEQ ID NO: 499)

45 ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCCCTACAAAATCAACCTGAAC  
 TCCAAGTGATGATATTCATCTTCTGTCTCCTACCTACATGCTAAGTATCTAGGAAATCTGT  
 ACTAATTACACCTCACTTACTAGACCCCCAACCAGACCCCCATGTATTCTCTCCG  
 GAATTTCTCCTTCTTAGAAAATTCCTTCACATCCATTTTATTTCCAGATTCTGACCCAGCA  
 TGACACAGGAAATAAAGTTATCAGCTTTGCTGGCTGCTTGACTCAGTATTTTGTGCTAT  
 50 ATTTCTTGGAGCTACCGAGTTTATCCCTGGCCTCCATGCTTATGATCGTATGTGCGGCA  
 TCTGCAAAACCCCTTGCAATTACCTGACTATTATGAGCAGCAGAGTCTGCATACAACCTAGTGTT  
 CTGCTCCTGGTTGGGGGGATTCTAGCAATCTTACCACCAATCATCATGACTGACCCAGGTA  
 GATTTCTGTGTCTCAACATCTGAATCACTATTACTGTGACTATGGGCGTCTCTGTGGAGCT  
 TGCGCTGCTCAGACACAAGCCTCTTAGAACTGATGGTCACTCTCTGGCCGTGTGACTCTC  
 55 ATGGTTACTCTGGTGCTGGTGACACTTTCTTACACATACATTATCAGGACTATTCTGAGGA  
 TCCCTTCTGCCAGCAAAGGACAAAGGCTTTTCCACTTGTCTCTCCACATGATTGTGTCATC

TCCCTCTCTTATGGCAGCTGCATGTTTATGTACATTAATCCCTTCTGCAAAAAGAGGAGGTG  
CTTTCAACAAAGGAATAGCTGTACTCATTACTTCGGTTACTCCCTTACTGAATCCCTTCATA  
TATACTTTAAGAAATCAGCAAGTGAAACAAGCTTTCAGGAGCTCAGTCAAAAAGATTGTG  
AAACTTTAA (SEQ ID NO: 500)

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**AOLFR274B sequences:**

MEFVFLAYSPCEPLHLSFLGVSLVYGLIITGNILVVSIIHTETCLCTSMYYFLGSLSGIEICYTAV  
VVPFILANTLQSEKTTILLGCATQMAFFIALGSADCFLLAAMAYDRYVAICHPLOYPLMLTLT  
CVHLLVVASVISGLFLSLQLVAFIESLPFCQAOGIEHFFCDVPPVMHVCAQSHIHEQSVLVAAIL  
AIAPVFFLITTSYTFIVAAALLKIHSAAGRHRAFSTCSSHLTVLLQYGCCAFMYLCPSSSYNPKQ  
DRFISLYYTLGTPLLNPLIYALRNSEMKGAUGRVLVRNCLSQNS (SEQ ID NO: 501)

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ATGGAATTGTGTCTCTGGCCCTATCCCTCTGCCGAGAAGTGCATATTCTGTCTCTCTCTGG  
GGTCAGCCCTGGTTTATGGTTTGATCATCACTGGGAACATTTCTATTGTGGTGTCCATTCA  
ACAGAAACCTGTCTATGCACATCCATGTACTATTCTCTGGCGAGCCCTTTCTGGGATTGAAA  
TATGCTACATGCAGTGGTGGTGGCCCATATCTCTGGCCAAACACCCTACAGTCAGAGAAGAC  
CATCATCTCTCTGGGCTGTGCCACCCAGATGGCTTTCTTATTGCACTGGGCAGTGGTGAT  
TGCTTCTCTCTGGGCTGTGCCATGTACCCGCTATGTGGCCATTGTCCACCCTGTGGCAGTA  
CCCTCTCTCATGACATTTGACTCTTTGTGTCCACTTGGTTGTGGCATCAGTCATCAGTGGTC  
TGTTCTGTCTTACAACCTGGTGGCCCTTCATCTTCTCTGCCATTCTCGCAGGCTCAGGGC  
ATTGAGCAGCTCTTTTGTGATGTGCCACCACTGCATGCATGTTGTTGTGTCTCAGATGCACAT  
TCATGAGCAGTCAGTGGTGGTGGCAGCCATACTAGCCATTGTGTGTGCTTCTCTCTCATC  
ACCACCTCTACACCTTCATAGTGGCTGTCTGTCTCAAGATCCACTCGGCTGTCTGGCCGCC  
ACCGGGCCTTCTCACCTGTCTTCTCCACCTCACTGTGGTGTCTGTGCAGTATGGCTGTCTGT  
GCCCTTCACTGTACCTGTGCCAGCTCCAGCTACAACCCCAAGCAAGATCGGTTTCATCTCAG  
TGGTGACACATTGGGAACCCCACTGTCTCAACCCCACTTATCTATGCCCTGAGGAACAGTGA  
GATGAAGGGGCCGTAGGGAGAGTTCTTACCAGGAAGTGCCTTCCAGAACAGCTAG  
(SEQ ID NO: 502)

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**AOLFR276B sequences:**

MGGFGTNISSTTSFTLTGFPPEMKGLEHWLAALLLLYIAISFLGNILILFIKEEQSLHQPMYYFLS  
LFSVNDLGVSFSTLPTVLAAVCFHAPETTFDACLQAMFFIHFSSWTEFGLLAMSFHDHYVAICNP  
LRATVLTVDVRVAHNGISIVIRSFVMVFLPFLKRLPFCKASVVLASHYGLCHADLIRLPWGD  
TINSMYGLFIVISAFGVDSLILLSYVLLHSVLAIASRGERLKLNTNCVSHIYAVLIFYVPMVSVS  
MVHRFGRHAPEYVYHKFMSLCTSNALPNYLFHQD (SEQ ID NO: 503)

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ATGGGGGGCTTTGGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCTTCCCTG  
AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTTCTGTGCTGCTTTATGCTATTCTCTT  
CCTGGGCAACATCCTCATCCTCTTTATCATAAAGGAAGAGCAGAGCTTGCACCAGCCAATG  
TACTACTTCTGTCTCTTTTCTGTTAATGACCTGGGTGTGCTCTTTCTACATTGCCCAT  
GTACTGGCTGCTGTGTGTTTTCATGCCCGCAGAGACAACTTTGATGCTCCTGCCCGCCAGA  
TGTTCTTCATCCACTTTTCTCTGGACAGAGTTTGGCACTCTACTGGCCATGAGTTTGGAC  
CACTATGTGCCCATCTGTAACCCGCTGCGCTATGGCCACAGTGCTCACTGATGTCCGTGGG  
CCCACAATGGCATATCCATTGTATCCGCACTGCTTCTGCAATGTAATCCCACTTCCCTTCCTC  
CTGAAGAGACTGCCCTTTCTGTAAGGCCAGTGTGGTACTGGCCAACTCCTACTGTCTGCATG  
CAGACCTGATTCGGCTGCCCTGGGGAGACATACCATCAACAGCATGTATGGCCTGTTCAT  
TGTCATCTCTGCCCTTTGGGTGATGATTCAGTCTCATCTCTCTCTCTTATGTGTCTTCTAC  
ATTCTGTGCTGGCCATTGGCTCCAGGGGTGAGAGGCTTAAGACACTCAACACATGTGTGTG  
ACATATCTATGCAGTGCTGTATCTTCTATGTGCCATTTGGTTAGTGTGTCCATGTTCATCGAT  
TGGGAGGACATGCTCTGAAATATGTGCACAAGTTCATGCTCTTTGTACCTCAAGTGCCT  
ACCCAATTATCTATTCATCAAGACTAA (SEQ ID NO: 504)

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**AOLFR311B sequences:**

MDWENCSSLTDFLLGITNNPEMKVTLFAVFLAVYIINFSANLGMVILIRMDYQLHTPMPYFLS  
HLSFCDLCYSTATGPKMLVDLLAKNKSIPFYGCALQFLVFCIFADSECLLLSVMAFDRYKAIINP  
LLYTVNMSSRVCYLLLTGVYLVGIADALIHMTLAFRLCFCGSNEINHFFCDIPPLLLSRSDTVQ

55

NELVLFTVFGFIELSTISGVFISYCYIILSVLEIHSABGRFKALSTCTSHLSAVAIFQGLLFMYFRP  
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVKALKLKNKILF (SEQ ID NO: 505)

ATGGAGCTGGGAAAATTTGCTCCTCATTAACTGATTTTTTCTCTTGGGAATTACCAATAACCC  
5 AGAGATGAAAGTGACCTATTGGCTGTATTCTTGGCTGTTTATATCATTAATTTCTCAGCAA  
ATCTTGGAAATGATAGTTTAAATCAGAATGGATTACCAACTTCACACCAATGATATTTCTT  
CCTCAGTCACTGTCTTTCTGTGATCTCTGCTATTCTACTGCAACTGGGCCCAAGATCTGGT  
TAGATCTACTTGGCAAGAACAAGTCAATACCCCTCTATGGCTGTGCTGTGCAATTTCTGGT  
CTTCTGTATCTTTGCAGATTCTGAGTGTCTACTGCTGTGAGTGTGGCCTTTGATCGGTACA  
10 AGGCCATCATCAACCCCTGCTCTATACAGTCAACATGTCTAGCAGATGTGCTATCTACT  
CTTGACTGGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCCTC  
CGCCTATGCTTCTGTGGGTCTAATGAGATTAATCATTTCTTCTGTGATATCCCTCCTCTCTT  
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTTAGTGTTATTCACCGCTTTTGGTTTTA  
TTGAAGTGAAGTACCAATTTCAAGAGTTTTCATTTCTTATTGTTATATCATCTCATCAGTCTTG  
15 GAGATACACTCTGCTGAGGGGAGGTTCAAAGCTCTCTACATGCACTTCCACITATCTG  
CGGTTGCAATTTCCAGGGAACCTCTGCTCTTATGATATTCCGGCCCAAGTCTTCTCTATTCT  
CTAGATCAAGATAAAATGACCTATTGTTTACACCTTGTGGTCCCATGTTGAACCCCT  
GATTTATAGCCTGAGGAAACAGGATGTGAAAGAGGCCCTGAAAAAACTGAAAAATAAAAT  
TTTATTTTAA (SEQ ID NO: 506)

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**AOLFR314 sequences:**

MEVKNCMVTEFILLIPHTEGLEMTLFLVFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG  
NLSVDFMGSSVTPKMLLYLMGLSRLSYKDCVQQLFFHFLGSIECLFTVMAYDRFTAICY  
PLRYTVIMNPRICVALAVGTWLLGCIHSSILSLTFTLPYCGPNEVDHFFCDIPALLPLACADTSL  
25 AQRVSFTNVGLISLVFLILLISYTRITISILSIRTEGRRRAFTCSAHLIALCAYGPILTLYQPT  
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVKTALKTILHRTGHVPES (SEQ ID NO: 507)

ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTTCATCCTTTTGGGAATCCCAACACACA  
GAGGGGCTGGAGATGACACTTTTGTCTTATTTCTTGCCCTTCTATGCCTGCACTCTACTGGG  
30 AAATGTGCTATCCTTGTGTCTGTATGTCTTCTGCTCGCTCCACACCACTATGATATCTT  
TCTCGGGAACCTGTCTGTGTTGACATGGGTTTCTCCTCAGTGACTTGTCCCAAAATGCT  
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTTCT  
TCTTCCATTTCTCGGGAGCATTGAGTGCCTCTGTGTTACGGTGATGGCCATGACCCGCTTC  
ACTGCCATCTGTTATCCTCTGCGATACACAGTCATCATGAACCCAAGGATCTGTGTGGCCC  
35 TGGCTGTGGGCACATGGCTGTTAGGGTGCAATTCATCCAGTATCTTGACCTCCTCACCTTC  
ACCTTGCCATCTGTGGTCCCAATGAAGTGGATCACTTCTTCTGTGACATTCAGCAGCTGTT  
GCCCTTGGCCTGTGCTGACACATCCTTAGCCAGAGGGTGAGCTTCACCAACGTGTGGCCTC  
ATATCTCTGTCTGCTTCTGTCTAATTTCTTTTATCCTACACTAGAATACCAATATCTATCTT  
AAGCATTCGTACAACACTGAGGGCGCTCGCCGTGCTTCCACCTGCAAGTCACTCACTT  
40 GCCATCCTCTGTGCCTATGGGCCCATCATCACTGTCTACCTGCAGCCACACCCAAACCCCA  
TGCTGGGAACCGTGGTACAATTTCTCATGAATCTGGTAGGACCAATGCTGAACCCCTTGAT  
CTATACTTGAAGAAATAAGGAAAGTAAAAACAGCCCTGAAAAACAATATGACAGGACGAG  
CCATGTCTCTGAGAGTTAG (SEQ ID NO: 508)

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**AOLFR324B sequences:**

MPIANDTQFHTSFFLLGIPGLEDVHIWIGFFPFSVYLIALLGNAAIFFVIQTEQSLHEPMYCYLA  
MLDSIDLSLSTATIPKMLGIFWFNIKEISFGGYLSQMFHFFFTVMESIVLVAMAFDRYIAICKPL  
WYTMILTSKIISLIAGIAVLRSLYMVIPLVFLLLRPFCHRIIPHTYCEHMGIARLACASIKVNM  
FGLGSILLLLDLVLIILSHIRLYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH  
50 DIPQYIHFLANLYVVPPTLNVPYGVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

ATGCCTATAGCTAACGACACCCAGTTCCTACTCTCTCATCTCTACTGCTGGGTATCCCAGG  
GCTAGAAGATGTGCACATCTGGATTGGATTCCCTTTTTTCTCTGTGATCTTATATGCACTCC  
TGGGAAATGCTGCTATCTTCTTGTGATCCAACTGAGCAGAGTCTCCATGAGCCCATGTGA  
55 CTACTGCTGGCCATGTGGATTCCATGACCTGAGCTTGTCTACGGGCACCATGTCCTCCAAA  
ATGCTGGGCACTTCTGTTCAATATCAAGGAAATATCTTTTGGAGGCTACCTTCTCAGA

5 TGTCTTCATCCATTCTTCACTGTCATGGAGAGCATCGTATTGGTGGCCATGGCCCTTGAC  
 CGCTACATTCGCATTGCAAAACCTCTTTGGTACACCATGATCCTCACCAGCAAAATCATCA  
 GCCTCATTTGCAGGCATTGCTGTCTGAGGAGCTTGATACATGGTCATTCCACTGGTGTCTCT  
 CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCAGATGG  
 GCATTGCCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT  
 TTCTCTCTTGTTATTTGGAATGTGCTCCTTATTATCTCTCCCATATCAGGATCCTCTATGCTGT  
 CTCTCGCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGCTCTCACATT  
 GGTGTTATCTTAGCCTTTTCTACACCAGCATTTTCTCTTCTTTACACACTGCTTTGGCCAT  
 10 GATATTCGCCAATATATCCACATTTTCTTGGCTAACTATATGTGGTGTCTCTCCCAACCT  
 CAATCCTGTAATCTATGGGGTCAGAACCAACATATTAGGGAGACAGTGCTGAGGATTTTC  
 TTCAAGACAGATCACTAA (SEQ ID NO: 510)

**AOLFR328 sequences:**

15 MALGNHSTITEFLLGLSADPNIRALLFVFLGIYLLTIMENLMLLLVIRADSCLHKPMYFFLSH  
 LSFVDLCFSSVIVPKMLENLLSQRKTISVEGCLAQVFFVFTAGTEACLLSGMAYDRHAAIRRP  
 LLYGQIMGKQLYMHVWGSWGLFLDALINVLLAVNMVFCIAKIIHHYSYEMPSLLPLSCSDI  
 SRSLLVLLCSTLLHGLGNFLVFLSYTRISTLSISSTSGRSKAFSTCSAHLTAVTLYYGSLRLHL  
 MPNSGSPIELFVSQYTVVTPMLNSLYSLKNKEVKALKRLEKLYQYTRR (SEQ ID NO: 511)

20 ATGGCCTTGGGGAATCACAGACCATCACCGAGTTCCTCCTCTGGGCTGTCTGCCGACC  
 CCAACATCCGGGCTCTGCTCTTTGTGCTGTTCTCGGGGATTTACCTCCTGACCAATAATGGA  
 AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCTTGCTCCATAAGCCCATGTATTTCT  
 TCCTGAGTCACCTCTCTTTTGTGATCTCTGCTTCTCTCAGTCATTGTGCCCAAGATGCTG  
 25 GAGAACCTCTGTCAAGAGGAAACCATTCAGTAGAGGGCTGCTGGCTCAGGTCTTCT  
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 35 TGCAATATACCAGACGTTGA (SEQ ID NO: 512)